
MAQ5RE4 (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 1 16:48:49 1996; MasPar time 42.82 Seconds
622.612 Million cell updates/sec

Tabular output not generated.

Title: >US-08-462-355-1

Description: (1-1446) from US08462355.seq

Perfect Score: 1446

N.A. Sequence: 1 ATGCGCTTTCTCTGCTGA.....AAAGAAATAGTACAACTGTG 1446
Comp: TACGCGAAGAGACGACACT.....TTTCTTATCATGTTGACAC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 30947 seqs, 9219370 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

n-issued
1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93
10:PCT94 11:PCT95

Statistics: Mean 8.992; Variance 4.572; scale 1.967

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	40	2.8	1872	9	PCT-US93-1 Sequence 39, Applicati	1.58e-12
2	38	2.6	2098	9	PCT-US93-1 Sequence 41, Applicati	3.48e-11
3	34	2.4	720	9	PCT-US93-1 Sequence 35, Applicati	1.47e-08
4	32	2.2	1610	10	PCT-US94-1 Sequence 7, Applicati	2.78e-07
5	32	2.2	1618	10	PCT-US94-1 Sequence 1, Applicati	2.78e-07
6	32	2.2	1618	10	PCT-US94-1 Sequence 3, Applicati	2.78e-07
7	29	2.0	120	9	PCT-US93-1 Sequence 3, Applicati	2.03e-05
8	28	1.9	1567	10	PCT-US94-1 Sequence 16, Applicati	8.21e-05
9	26	1.8	1265	4	US-07-816- Sequence 3, Applicati	1.26e-03
c 10	24	1.7	105	4	US-07-865- Sequence 13, Applicati	1.75e-02

11	24	1.7	1307	11	PCT-US95-0	Sequence 1, Applicati	1.75e-02
12	25	1.7	1317	9	PCT-US93-1	Sequence 45, Applicati	4.75e-03
13	25	1.7	1351	4	US-07-816-	Sequence 5, Applicati	4.75e-03
14	24	1.7	1572	4	US-08-041-	Sequence 5, Applicati	1.75e-02
15	25	1.7	1737	4	US-08-202-	Sequence 4, Applicati	4.75e-03
16	25	1.7	1737	10	PCT-US94-0	Sequence 2, Applicati	4.75e-03
17	23	1.6	105	4	US-07-865-	Sequence 13, Applicati	6.30e-02
18	23	1.6	1634	4	US-07-816-	Sequence 1, Applicati	6.30e-02
19	23	1.6	1796	4	US-07-816-	Sequence 11, Applicati	6.30e-02
c 20	22	1.5	84	10	PCT-US94-0	Sequence 25, Applicati	2.20e-01
21	22	1.5	652	8	PCT-US92-0	Sequence 2, Applicati	2.20e-01
22	21	1.5	1106	11	PCT-US95-0	Sequence 4, Applicati	7.42e-01
23	21	1.5	1106	8	PCT-US92-0	Sequence 5, Applicati	7.42e-01
24	21	1.5	1161	9	PCT-US93-1	Sequence 31, Applicati	7.42e-01
25	21	1.5	1176	11	PCT-US95-0	Sequence 2, Applicati	7.42e-01
26	22	1.5	1200	11	PCT-US95-0	Sequence 1, Applicati	2.20e-01
27	22	1.5	1200	8	PCT-US92-0	Sequence 1, Applicati	2.20e-01
28	21	1.5	1244	4	US-07-816-	Sequence 7, Applicati	7.42e-01
29	22	1.5	1296	4	US-07-816-	Sequence 9, Applicati	2.20e-01
30	21	1.5	1510	3	US-07-759-	Sequence 4, Applicati	7.42e-01
31	21	1.5	1748	4	US-08-202-	Sequence 8, Applicati	7.42e-01
32	21	1.5	1883	4	US-08-202-	Sequence 2, Applicati	7.42e-01
33	21	1.5	1901	9	PCT-US93-1	Sequence 43, Applicati	7.42e-01
34	21	1.5	1933	10	PCT-US94-0	Sequence 1, Applicati	7.42e-01
35	21	1.5	2254	9	PCT-US93-1	Sequence 27, Applicati	7.42e-01
36	21	1.5	2830	9	PCT-US93-0	Sequence 1, Applicati	7.42e-01
37	21	1.5	2830	3	US-07-882-	Sequence 1, Applicati	7.42e-01
38	20	1.4	1584	8	PCT-US92-0	Sequence 5, Applicati	2.42e+00
39	20	1.4	3259	11	PCT-US95-0	Sequence 1, Applicati	2.42e+00
c 40	20	1.4	4100	8	PCT-US92-0	Sequence 3, Applicati	2.42e+00
c 41	20	1.4	6375	8	PCT-US92-0	Sequence 5, Applicati	2.42e+00
c 42	20	1.4	6375	8	PCT-US92-0	Sequence 5, Applicati	2.42e+00
43	20	1.4	8043	10	PCT-US94-0	Sequence 1, Applicati	2.42e+00
c 44	20	1.4	8252	4	US-08-046-	Sequence 15, Applicati	2.42e+00
c 45	20	1.4	8252	9	PCT-US93-1	Sequence 15, Applicati	2.42e+00

ALIGNMENTS

RESULT 1

ID PCT-US93-11153-39 STANDARD; DNA; UNC; 1872 BP.

AC xxxxx

DT 01-JAN-1900

DE Sequence 39, Application PC/TUS9311153.

CC Sequence 39, Application PC/TUS9311153

CC GENERAL INFORMATION:

CC APPLICANT: Godiska, Ronald

CC APPLICANT: Gray, Patrick W.

CC APPLICANT: Schweikart, Vicki L.

CC TITLE OF INVENTION: Novel Seven Transmembrane Receptors

CC NUMBER OF SEQUENCES: 64

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bicknell

CC STREET: 6300 Sears Tower, 233 South Wacker Drive

CC CITY: Chicago

CC STATE: Illinois

CC COUNTRY: USA

CC ZIP: 60606

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/111153
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/977,452
CC FILING DATE: 17-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31794
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 474-6300
CC TELEFAX: (312) 474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 39:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1872 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 202..1341
SQ Sequence 1872 BP; 328 A; 592 G; 491 C; 456 T; 5 other;
Query Match 2.8%; Score 40; DB 9; Length 1872;
Best Local Similarity 70.0%; Pred. No. 1.58e-12;
Matches 70; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Db 484 TGGCCCTTTGGGACCTCTTCCAGCTCAGCAGCTACCTCATCTTCTCAACATGTAC 543
Qy 262 TGGCCCTCAGCGAGGTCTCTCAAGCTCATCCCTCCATCATCTCTCAACATGTTT 321
Db 544 GCACGGCTCTTGCTCAGCGGCTCAGCTCAGCTCGCCGCT 583
Qy 322 GCGAGTGTCTTCTGCTTACTGCCATTAGCGCTGATGCGCT 361
RESULT 2
ID PCT-US93-11153-41 STANDARD; DNA; UNC; 2098 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 41, Application PC/TUS9311153.
CC Sequence 41, Application PC/TUS9311153
CC GENERAL INFORMATION:
CC APPLICANT: Godiska, Ronald
CC APPLICANT: Gray, Patrick W.
CC APPLICANT: Schweikart, Vicki L.
CC TITLE OF INVENTION: Novel Seven Transmembrane Receptors
CC NUMBER OF SEQUENCES: 64
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/111153
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/977,452
CC FILING DATE: 17-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31794
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 474-6300
CC TELEFAX: (312) 474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 41:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 2098 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 551..1681
SQ Sequence 2098 BP; 371 A; 594 C; 671 G; 462 T; 0 other;
Query Match 2.6%; Score 38; DB 9; Length 2098;
Best Local Similarity 61.0%; Pred. No. 3.48e-11;
Matches 105; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
Db 921 TCACATGTACGCCAGCGTCTGCTTATCAGCGGCATGCTAGACCGCTCAGTGGCGG 980
Qy 311 TCACATGTTGGCAGTGTCTTCTGCTTACTGCCATTAGCGCTGCTTGTGG 370
Db 981 TGGCCCGCCCTTTGTGCCAGAGCTACGACCAAGCGCATGCCCGCGGTGCTGG 1040
Qy 371 TATTCAGCCAATCTGGTGTAGAAATCATGCAATGTAGGATGGCCCTGCTATCTGTG 430
Db 1041 CAGGCATCTGGGTGTGCTGCTTTCTGCTGGCCACACCCGCTCTCGCGGTACCG 1092
Qy 431 CATGTATCTGGGTGGTGGCTTTTGTGTCGATTCTGCTGTCGTGACCG 482
RESULT 3
ID PCT-US93-11153-35 STANDARD; DNA; UNC; 720 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 35, Application PC/TUS9311153.
CC Sequence 35, Application PC/TUS9311153
CC GENERAL INFORMATION:
CC APPLICANT: Godiska, Ronald
CC APPLICANT: Gray, Patrick W.
CC APPLICANT: Schweikart, Vicki L.
CC TITLE OF INVENTION: Novel Seven Transmembrane Receptors
CC NUMBER OF SEQUENCES: 64
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA

CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/11153
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/977,452
CC FILING DATE: 17-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302
CC REFERENCE/DOCKET NUMBER: 31794
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 474-6300
CC TELEFAX: (312) 474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 35:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 720 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 258..719
SQ Sequence 720 BP; 160 A; 176 C; 154 G; 230 T; 0 other;

Query Match 2.4%; Score 34; DB 9; Length 720;
Best Local Similarity 66.0%; Pred. No. 1.47e-08;
Matches 70; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db 546 GCACTGGCGGACGGGCTCTTCTGTGCAAGGAGCTCTACATGATCGGTCAAT 605
||||| ||||| ||| ||||| ||||| || |||| |||| || ||||
Qy 256 GGACAGTGGCCCTACGGCAGGTTCTATGCAAGCTCATCCCTCCATCATTTGCTCAAC 315

Db 606 ATGCATGCAAGTCTCTCTGCTACTGATGATGATGTTGACCGCT 651
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 316 ATCTTTGCAGTCTCTCTCTCTACTGCGATTAGCTGGATGGCT 361

RESULT 4
ID PCT-US94-10358-7 STANDARD; DNA; UNC; 1610 BP.

AC xxxxxx
DT 01-JAN-1900
DE Sequence 7, Application PC/TUS9410358.
CC Sequence 7, Application PC/TUS9410358
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P. O. Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
CC SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/10358
CC FILING DATE: Concurrently herewith
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/120,601
CC FILING DATE: 13 SEPTEMBER 1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WILSON, MARK B.
CC REGISTRATION NUMBER: 37,259
CC REFERENCE/DOCKET NUMBER: INDA005P--
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (512) 418-3000
CC TELEFAX: (713) 789-2679
CC TELEX: 79-0924
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1610 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other;

Query Match 2.2%; Score 32; DB 10; Length 1610;
Best Local Similarity 83.3%; Pred. No. 2.78e-07;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 1092 TGGTGGTGGCTGCTGCTTCATCGTCTGCTGCACTCCCATTCACATTT 1139
||||| ||||| ||||| || ||||| ||||| ||||| |||||
Qy 1139 TGGTGGTGGCTGCTGCTTTCTGCTGCTGCACTCCATACCATTT 1186

RESULT 5
ID PCT-US94-10358-1 STANDARD; DNA; UNC; 1618 BP.

AC xxxxxx
DT 01-JAN-1900
DE Sequence 1, Application PC/TUS9410358.
CC Sequence 1, Application PC/TUS9410358
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: P. O. Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
CC SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/10358
CC FILING DATE: Concurrently herewith
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:


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CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/04464
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wallen III, John W.
CC REGISTRATION NUMBER: 35,403
CC REFERENCE/DOCKET NUMBER: 19202
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-3905
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1307 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC Sequence 1307 BP; 282 A; 400 C; 306 G; 319 T; 0 other;
SQ
Query Match 1.7%; Score 24; DB 11; Length 1307;
Best Local Similarity 71.4%; Pred.No. 1.75e-02;
Matches 40; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 974 GTGCTGGCTTCCTGCTGCTGGGCCCTTACACATCTTTTGCCTCTCTGGAATT 1029
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QY 1147 GTGGCTGCTCTTTCTGTCTGGAGCTCCATACACATTTGGGGAGCTCGTGCA 1202

RESULT 12
ID PCT-US93-11153-45 STANDARD; DNA; UNC; 1317 BP.
AC xxxxxx
AD 01-JAN-1900
DT
DE Sequence 45, Application PC/TUS9311153.
CC Sequence 45, Application PC/TUS9311153
CC GENERAL INFORMATION:
CC APPLICANT: Godiska, Ronald
CC APPLICANT: Gray, Patrick W.
CC APPLICANT: Schweikart, Vicki L.
CC TITLE OF INVENTION: Novel Seven Transmembrane Receptors
CC NUMBER OF SEQUENCES: 64
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/11153
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/977,452
CC FILING DATE: 17-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Noland, Greta E.
CC REGISTRATION NUMBER: 35,302

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CC REFERENCE/DOCKET NUMBER: 31794
CC TELEPHONE INFORMATION:
CC TELEPHONE: (312) 474-6300
CC TELEFAX: (312) 474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 45:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1317 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 201..1211
SQ Sequence 1317 BP; 332 A; 342 C; 265 G; 378 T; 0 other;

Query Match 1.7%; Score 25; DB 9; Length 1317;
Best Local Similarity 61.7%; Pred.No. 4.75e-03;
Matches 66; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db 452 GCGAAACTGGTACTTTGGGAAGCTTCCTATCGAAGCGAGTCCTATGTCATCTACACAGTCAA 511
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Qy 255 GGGACAGTGGCCCTAGCGCAGGTTCTCTAGCAGCTCATCCCTCCATCATCTCCTCAA 314

Db 512 CCTCTACAGAGTGTCTCATCTGGCCTTCATCAGTCTGGACCGCT 558
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Qy 315 CATGTTGGCAGTGTCTCTGCTTACTGCCATTAGCCTGGATCGCT 361

RESULT 13
ID US-07-816-283-5 STANDARD; DNA; UNC; 1351 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 5, Application US/07816283.
CC Sequence 5, Application US/07816283
CC Patent No. 5436155
CC GENERAL INFORMATION:
CC APPLICANT: Bell, Graeme I.
CC APPLICANT: Yamada, Yuichiro
CC APPLICANT: Saino, Susumu
CC TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Arnold, White & Durkee
CC STREET: PO Box 4433
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77210
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/816,283
CC FILING DATE: 19911231
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: McDaniel, C. Steven
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 713-787-1400
CC TELEFAX: 713-789-2679

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CC	REGISTRATION NUMBER:	30,300	
CC	REFERENCE/DOCKET NUMBER:	P-8700-23781	
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE:	(202) 887-0400	
CC	TELEFAX:	(202) 835-0605	
CC	TELEX:	440706	
CC	INFORMATION FOR SEQ ID NO: 5:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH:	1572 base pairs	
CC	TYPE:	nucleic acid	
CC	STRANDEDNESS:	double	
CC	TOPOLOGY:	linear	
CC	MOLECULE TYPE:	cDNA	
CC	ORIGINAL SOURCE:		
CC	ORGANISM:	Homo sapiens	
CC	TISSUE TYPE:	Placental	
CC	SQ Sequence 1572 BP; 424 A; 359 C; 329 G; 460 T; 0 other;		
	Query Match	1.7%;	Score 24; DB 4; Length 1572;
	Best Local Similarity	62.2%;	Pred. No. 1.75e-02;
	Matches	61; Conservative	0; Mismatches 37; Indels 0; Gaps 0;
Db	519	TGGCCCTTTGGCAATTACCTATTGATGATTGCTTCACCAGCGCTCAGTTTCAACCTGTAC	578
Qy	262	TGGCCCTACGGCAGGTTCCGATGCAAGCTCATCCCTCCATGTCATTGTCCTCAACATGTTT	321

Qy	262	TGGCCCTAGGCGAGGTTCTGATGAAGCTCATCCCTCCATATTGCTCAACATGTTT	321
Db	579	GCTAGTGTGTTCTACTACGTGCTCTCAGCATTTGATCG	616
Qy	322	GCCAGTGTCTTCTGTTACTGCCATTAGCCTGGATCG	359
RESULT	15		
ID	US-08-202-056-4	STANDARD; DNA; UNC; 1737 BP.	
AC	xxxxxx		
DT	01-JAN-1900		
DE	Sequence 4,	Application US/08202056.	
CC	Sequence 4,	Application US/08202056	
CC	Patent No. 5440021		
CC	GENERAL INFORMATION:		
CC	APPLICANT:	Chuntharapai, Anan	
CC	APPLICANT:	Hebert, Caroline	
CC	APPLICANT:	Kim, Kyung Jin	
CC	APPLICANT:	Lee, James	
CC	TITLE OF INVENTION:	Antibodies to Human IL-8 Type B Receptor	
CC	NUMBER OF SEQUENCES:	8	
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE:	Genentech, Inc.	
CC	STREET:	460 Point San Bruno Blvd	
CC	CITY:	South San Francisco	
CC	STATE:	California	
CC	COUNTRY:	USA	
CC	ZIP:	94080	
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE:	5.25 inch, 360 Kb floppy disk	
CC	COMPUTER:	IBM PC compatible	
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS	
CC	SOFTWARE:	patin (Genentech)	
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER:	US/08/202,056	
CC	FILING DATE:	25-FEB-1994	
CC	CLASSIFICATION:	436	
CC	PRIOR APPLICATION DATA:		
CC	PRIOR APPLICATION NUMBER:	07/677211	
CC	FILING DATE:	29-MAR-1991	

• • •

May 1 16:41

US-08-462-355-1.rmi

17

ATTORNEY/AGENT INFORMATION:

CC NAME: Love, Richard B.
CC REGISTRATION NUMBER: 34,659
CC REFERENCE/DOCKET NUMBER: 706P3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-5530
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1737 bases
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear

SQ Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T; 0 other;

Query Match 1.7%; Score 25; DB 4; Length 1737;
Best Local Similarity 61.7%; Pred. No. 4.75e-03;
Matches 66; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

D6 387 GCGAACTGCTACTTTGGAACTTCTATGCAAGGCAGTCATGTCTACACAGTCAA 446
||| ||| || ||| ||||| ||||| ||| ||||| |||||
QY 255 GGCACAGTGGCCCTACGGCAGGTTCTATGCAAGCTCATCCCTCATCATTTGCTCTCAA 314
||| ||||| ||| ||| ||| ||||| |||||
D6 447 CCTCTACAGCAGTGTCTCATCTGCGCTTCATCATGCTGGACCGCT 493
||| ||||| ||| ||| ||| ||||| |||||
QY 315 CATGTTGGCAGTGTCTCTCTGCTTACTGTCATAGCCATGACCTGGATCGCT 361

Search completed: Wed May 1 16:49:35 1996
Job time : 46 secs.

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

Statistics: Mean 11.364; Variance 1.885; scale 6.028

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		ID	Description	Pred. No.	
		Match	Length				
1	421	29.1	484	55	R77881	y17h05.r1 Homo sapie	0.00e+00
2	358	24.8	471	60	R92269	yq06g01.r1 Homo sapie	0.00e+00
3	358	24.8	471	116	HS269192	yq06g01.r1 Homo sapie	0.00e+00
4	248	17.2	256	86	T91438	yel0d06.r1 Homo sapie	0.00e+00
5	246	17.0	319	75	T49050	yb08e05.r1 Homo sapie	0.00e+00
6	212	14.7	334	34	R01558	ye79h02.r1 Homo sapie	0.00e+00
7	83	5.7	297	50	R58715	G4756 Homo sapiens cd	3.31e-125
8	68	4.7	349	33	R04676	yf09s01.r1 Homo sapie	9.09e-92
9	31	2.1	466	38	R15256	yf89d01.r1 Homo sapie	8.03e-18
10	27	1.9	183	56	R81583	yj04b04.r1 Homo sapie	2.31e-11
11	28	1.9	238	32	M78084	EST01672 Homo sapiens	6.32e-13
12	26	1.8	497	86	T90501	ye15a04.s1 Homo sapie	7.70e-10
13	24	1.7	249	12	H29103	ym31f07.r1 Homo sapie	6.35e-07
14	23	1.6	198	7	H14008	EST00034 Homo sapiens	1.55e-05
15	23	1.6	205	7	H14012	EST00038 Homo sapiens	1.55e-05
16	23	1.6	232	27	H5C2UF111	H. sapiens partial cd	1.55e-05
17	23	1.6	355	101	H75904	yu08f03.r1 Homo sapie	1.55e-05
18	23	1.6	325	125	HS904230	yu08f03.r1 Homo sapie	1.55e-05
19	23	1.6	388	76	T53360	ya8d05.s1 Homo sapie	1.55e-05
20	23	1.6	421	121	HS609197	yq72f10.r1 Homo sapie	1.55e-05
21	23	1.6	421	62	R98609	yq72f10.r1 Homo sapie	1.55e-05
22	23	1.6	431	92	G09547	human STS CHLC.GCT7D1	1.55e-05
23	23	1.6	452	57	R82424	yf18h04.r1 Homo sapie	1.55e-05
24	23	1.6	475	42	R31127	yf16b05.r1 Homo sapie	1.55e-05
25	23	1.6	508	105	H87900	yw16f03.r1 Homo sapie	1.55e-05
26	23	1.6	508	125	HS900247	yw16f03.r1 Homo sapie	1.55e-05
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28	22	1.5	203	117	HS324189	yt70e04.s1 Homo sapie	3.33e-04
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30	22	1.5	254	26	H5C2JG042	H. sapiens partial cd	3.33e-04
31	22	1.5	270	27	H5C35C062	H. sapiens partial cd	3.33e-04
32	22	1.5	299	69	T24086	seq2272 Homo sapiens	3.33e-04
33	21	1.5	301	129	RS5001	EST107661 Rattus sp.	6.26e-03
34	22	1.5	316	113	HS04115	EST56443 Homo sapiens	3.33e-04
35	22	1.5	316	71	T33041	EST56443 Homo sapiens	3.33e-04
36	22	1.5	324	65	T02691	0047M7 Plasmodium fal	3.33e-04
37	22	1.5	324	128	PF691	0047M7 Plasmodium fal	3.33e-04
38	22	1.5	347	42	R30721	F9614 Homo sapiens cd	3.33e-04
39	22	1.5	352	115	HS148G05B	Human fetal brain cDN	3.33e-04
40	22	1.5	352	30	HUM148G05B	Human fetal brain cDN	3.33e-04
41	22	1.5	365	79	T66281	yc78a06.s1 Homo sapie	6.26e-03
42	22	1.5	386	8	H14301	ym63c04.r1 Homo sapie	3.33e-04
43	22	1.5	445	65	T03650	IB671 Homo sapiens cd	3.33e-04
44	22	1.5	452	40	R22110	yh25f05.r1 Homo sapie	3.33e-04
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ALIGNMENTS

RESULT	1				
LOCUS	R77881	484 bp	mRNA	EST	07-JUN-1995



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch nn· n.a. - n.a. database search, using Smith-Waterman algorithm

```
Run on: Wed May 1 16:38:24 1996; MasPar time 589.87 Seconds
881.274 Million cell updates/sec
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Tabular output not generated.

Title: >US-08-462-355-1

Description: (1-1446) from US08462355.seq

Perfect Score: 1446

Sequence: 1 ATGGCGTCTTTCTCTGCTGA.....AAAGAAATAGTACAACTGTG 1446
Comp: TACCGAGAAAGACAGCGACT.....TTTCTTTATCATGTTGCACAC

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1-EST1 2-EST2 3-EST3 4-EST4 5-EST5 6-EST6 7-EST7 8-EST8
9-EST9 10-EST10 11-EST11 12-EST12 13-EST13 14-EST14
15-EST15 16-EST16 17-EST17 18-EST18 19-EST19 20-EST20
21-EST21 22-EST22 23-EST23 24-EST24 25-EST25 26-EST26
27-EST27 28-EST28 29-EST29 30-EST30 31-EST31 32-EST32
33-EST33 34-EST34 35-EST35 36-EST36 37-EST37 38-EST38
39-EST39 40-EST40 41-EST41 42-EST42 43-EST43 44-EST44
45-EST45 46-EST46 47-EST47 48-EST48 49-EST49 50-EST50
51-EST51 52-EST52 53-EST53 54-EST54 55-EST55 56-EST56
57-EST57 58-EST58 59-EST59 60-EST60 61-EST61 62-EST62
63-EST63 64-EST64 65-EST65 66-EST66 67-EST67 68-EST68
69-EST69 70-EST70 71-EST71 72-EST72 73-EST73 74-EST74
75-EST75 76-EST76 77-EST77 78-EST78 79-EST79 80-EST80
81-EST81 82-EST82 83-EST83 84-EST84 85-EST85 86-EST86
87-EST87 88-EST88 89-EST89 90-EST90 91-EST91 92-EST92
93-EST93 94-EST94 95-EST95 96-EST96 97-EST97 98-EST98
99-EST99 100-EST100

Database:

95: enEST1 96: enEST2 97: enEST3 98: enEST4 99: enEST5
100: enEST6 101: enEST7 102: enEST8 103: enEST9 104: enEST10
105: enEST11 106: enEST12 107: enEST13 108: enEST14 109: enEST15
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504: enEST410 505: enEST

DEFINITION y17h05.rl Homo sapiens cDNA clone 145305 5' similar to SP:BLRI_HUMAN P32302 BURK1T1T S LYMPHOMA RECEPTOR ;.
ACCESSION R77881
KEYWORDS EST.
SOURCE human clone=145305 library=Soares placenta Nb2HP vector=p773D (Pharmacia) with a modified polylinker host=DRI10B (ampicillin resistant) primer=M13RP1 Rsite=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo (dT) primer [5'-ACTCGAAGAAATTCGCGCCGACGAGAAATTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 484)
HILLIER, L., CLARK, N., DUBUQUE, T., ELLISTON, K., HAWKINS, M.,
HOLMAN, M., HULTMAN, M., KUCABA, T., LE, M., LENNON, G., MARRA, M.,
PARSONS, J., RIFKIN, L., ROHIFING, T., SOARES, M., TAN, F.,
TREVASKIS, E., WATERSTON, R., WILLIAMSON, A., WOHLDMANN, P. and
WILSON, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

Contact: Wilson RK
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu

NCBI gi: 852991	
Location/Qualifiers	
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/clone="145305"	
/note="human"	
BASE COUNT	107 a 117 c 111 g 147 t 2 others
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Best Local Similarity	96.9%; Pred. No. 0.00e+00;
Matches 469; Conservative	0; Mismatches 8; Indels 7; Gaps 7;

181	ctgtgtacagcttcattgtctctcgaatgcaaaaggggcgccttcgccaaagtctcagagca	240
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Qy		
241	aaaccttcgaagtcgccgtgggtggtagctgctcttcttctgtctgtagctccataacc	300
Db		
1121	AAACCTTTGACGTGGCGTGGTGGTGCTCTTCTCTGTCTGTGGACTCCATACC	1180
Qy		
301	acattttggggagtcctgttcattgcttactgaccagaagaactcccttgggggaaaaactc	360
Db		
1181	ACAATTG-GGGAGTCCCTGT-CATTGCTTACTGACCCAGAACTCCCTTTGGGGAAAA-CTC	1237
Qy		
361	tgatgttctcggggtacangtatgcattgctctagcatctgccaaattagtgtcttaatcc	420
Db		
1238	TGATGTCCTGGG-AFCATGATGCAATTGCTCTAGCAATCGCCAAAT-AGTGTCTTTAATCC	1295
Qy		
421	cttcnntt-atgccctctttgggaagaattttaggaggaggaagcagg-agtccattcaggg	478
Db		
1296	CTTCCTTTATGCCCCTCTTGGGAAAAGATTTTAGGAAGAAAGCAAGCAGTCCATTCAGGG	1355
Qy		
479	attt 482	
Db		
1356	AAAT 1359	
Qy		

2	RESULT					
	Locus	R92269	471 bp	mRNA	EST	25-AUG-1995
	DEFINITION	yQ06g01.r1 Homo sapiens cDNA clone 196176 5'.				
	ACCESSION	R92269				
	KEYWORDS	EST.				
	SOURCE	human clone=196176 library=Soares fetal liver spleen INFUS vector=pT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 Reitel= Pac I ReiteZ=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAGAAATTAAATGAGCTCTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.				

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 471)

REFERENCE

REFERENCE AUTHORS	TITLE JOURNAL
1 (Bases 1 to 471)	
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, K., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.	The WashU-Merck EST Project Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 341
Source: IMAGE Consortium. L1NL

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 256)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence atops: 216
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 723351 Location/Qualifiers
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/note="human"
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Best Local Similarity 99.2%; Pred. No. 0.00e+00;
Matches 254; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Db 1 agctgtccctagcgtctcagcaattcctcagagctcgtgagctaccacaaggttcc 60
|||||
Qy 884 AGCTGTCCTAGCGCTTCTAGCAATTCCTTACAGCTCTGAGCTACCAAGGTTCC 943
|||||
Db 61 aggattattacaatttagccaatccagatgacgatcaagtgccacacccctcgtgg 120
|||||
Qy 944 AGGATTATTACATTTAGGCCAATTCACAGATGACGATCAAGTGCCACACCCCTCGTG 1003
|||||
Db 121 gcataacgatcactaggtcgtggtgttctcagagctcgtggtcgttatcatgatgcc 180
|||||
Qy 1004 -CAATAACGATACATAGCGTAGGTGGGTTCTCTGCGCCCTCTTTATCATGATAGCC 1062
|||||
Db 181 tgttcagcttcattgtctcgaatgcaaggccgcttcctcccaagctcagagcaaa 240
|||||
Qy 1063 TGTTCACGTTCTATGTTCTCCGATGCGAAGGGGGCGCTTCGCCAAGTCTCAGACAAA 1122
|||||
Db 241 accttcgagtgccg 256
|||||
Qy 1123 ACCTTCGAGTGGCG 1138

RESULT 5
LOCUS T49050 319 bp mRNA EST 08-FEB-1995
DEFINITION yb08e05.r1 Homo sapiens cDNA clone 70592 5'.
ACCESSION T49050
KEYWORDS EST.
SOURCE human clone=70592 Library=Stratagene placenta (#937225)

vector=pluescript SK- host=SO1R cells (kanamycin resistant)
primer=M13RP1 Rsite=EcoRI Rsite2=XhoI Placental tissue from a
Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.2 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence:
5'-CTCCAGCTTTTTTTTTTTTTTTTTT-3'.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 319)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Other ESTs: yb08e05.s1

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence atops: 268

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 650910 Location/Qualifiers
source 1..319
/organism="Homo sapiens"
/clone="70592"
/note="human"
BASE COUNT 85 a 80 c 55 g 99 t
ORIGIN

Query Match 17.0%; Score 246; DB 75; Length 319;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 264; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

Db 11 ctcttgaaacattgttcagccgcttgagaaatgaatgataggttagatcctctctt 70
|||||

Qy 587 CTCITGAAACATTTTCAGCGCCTCGAGAAATGATAGTTAGTCTCTCTT 646
|||||

Db 71 tcacaacaaatgatcatccttgagacgtccccactgtcttccaacctcaaacattcaaa 130
|||||

Qy 647 TCCAAACAAATGATCATCTCTGGACAGTCCCACTGTCTTCCACCTCAAAATTCAAA 706
|||||

Db 131 gacctctgcagattcactccctaggggttctcgtaggttaacaagtcaaaatctgtatt 190
|||||

Qy 707 GACCTTCTGCACATTACCTCCCTAGGGGTTCTGCTAGGTTAAACAGTCAAAATCTGTATT 766
|||||

Db 191 ctaatgtatttaaacctgctgatgtggtctcacctaaaaatccccagtggggttctctatt 250
|||||

Qy 767 CTAATGTATTTAAACCTGCTGATGTGCTCACTAAATCCCAAGTGGG-TTTCCTATT 825
|||||

Db 251 tgaagatcacggaacaccagccactgg 277
|||||

Qy 826 -GAAGATCAGC-AAACCAGCCCACTGG 850
|||||

May 1 16:40

US-08-462-355-1.rst

9

LOCUS R01558 334 bp mRNA EST 31-MAR-1995
DEFINITION ye79h02.r1 Homo sapiens cDNA clone 123987 5'.
ACCESSION R01558
KEYWORDS EST.
SOURCE human clone=123987 library=Soares fetal liver spleen INFLS

vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RPI Reitel=Pas I Reitel=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGAGACATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 334)

REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 259
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 751294

FEATURES
source Location/Qualifiers
1..334
/organism="Homo sapiens"
/clone="123987"
/note="human"

BASE COUNT 95 a 68 c 84 g 84 t 3 others
ORIGIN

Query Match 14.7%; Score 212; DB 34; Length 334;
Best Local Similarity 99.5%; Pred. No. 0.00e+00;
Matches 218; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ggaactctgatgctctggatcatgtatgctctgcttagcatctgcacatgttgt 60
|||||
Qy 1229 GGAAGAACTCTGATGCTCTGGATCATGTATGCATTGCTTAGCATCTGCCAATAGTTGCT 1288
|||||
Db 61 ttaatccctctcttatgcctcttgggaaagattttaggagaagcaggcagctcca 120
|||||
Qy 1289 TTAATCCCTCTCTTATGCCCTCTTGGGAAGATTTTAGAGAGAAGCAGGAGCTCCA 1348
|||||
Db 121 ttcagggaattctggaggcagctctcagtgaggangctcacacgttccacccactgtccc 180
|||||
Qy 1349 TTCAGGGAATTCCTGGAGGAGCAGCTCTCAGTGAGGA-CCTCACAGCTTCCACCCACTGTCCC 1407
|||||
Db 181 tcaacaatgtcatttcagaaagaatagtacaaactgtg 1919

May 1 16:40

US-08-462-355-1.rst

10

Qy 1408 TCACACAACTGTCATTTTCAGAGAAGAAATAGTACAACTGTG 1446
|||||

RESULT 7

LOCUS R58715 297 bp mRNA EST 23-MAY-1995
DEFINITION G4756 Homo sapiens cDNA clone G4756 5' end.
ACCESSION R58715
KEYWORDS EST.

SOURCE human clone=G4756 library=Fetal heart vector=Lambda gt22 host=E. coli Y1090 primer=GGTGGCCGACCACTCTCGAGCC Reitel=NotI Reitel=SalI mRNA was purified from human fetal hearts (10-12 weeks). cDNA was constructed using a NotI-Oligo dT adaptor-primer. SalI adaptors were ligated, followed by digestion with NotI, for direction cloning into predigested lambda gt22. Method is described in J. Mol. Cell. Cardiol. (1994) 26, 1329-1333).

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonadata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 297)

REFERENCE

AUTHORS Hwang,D.M., Fung,Y.W., Wang,R.X., Laurensen,C.M., Ng,S.H., Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C.
Analysis of Expressed Sequence Tags (ESTs) from Fetal and Adult Heart cDNA Libraries
Unpublished (1995)

JOURNAL

COMMENT

Contact: Liew CC
Molecular Cardiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 4169785650
Email: liewcc@utcc.utoronto.ca.

NCBI gi: 828773

FEATURES
source Location/Qualifiers
1..297
/organism="Homo sapiens"
/clone="G4756"
/note="human"

BASE COUNT 85 a 63 c 80 g 69 t
ORIGIN

Query Match 5.7%; Score 83; DB 50; Length 297;
Best Local Similarity 91.5%; Pred. No. 3.31e-125;
Matches 108; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Db 1 ttttagaagagcaggcagtcattcagggaattctggaggcagccttcagtgaggg 60
|||||

Qy 1323 TTTTAGGAGAGAACGACGACCTCCATTCAGGGAATTCGGAGGACGCTTCAGTCGAGGA 1382
|||||

Db 61 gg--acacgttccaccactgtccctcaa--caatgtcatttcagagagagatagta 115
| |||||

Qy 1383 GCTCACAGTCTCCACCACCTGTCCCTCAACAAATGTCATTTCAGAAAGAAATAGTACA 1440
|||||

RESULT 8

LOCUS R06476 349 bp mRNA EST 03-APR-1995
DEFINITION yf09h01.r1 Homo sapiens cDNA clone 126313 5' similar to gb:M60626
ACCESSION R06476
KEYWORDS EST.
FRMT-LHE RECEPTOR (HUMAN).

SOURCE human clone=126313 library=Soares fetal liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker host=pDH10B (ampicillin resistant) primer=M13Rp1 Reitel-Pac I Reitel2-Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAGACATTAATTAAGATCTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 I vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 349)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, C., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

Contact: Wilson RK
Washington EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 315
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

```
NCBI gi: 757096
FEATURES
            Location/Qualifiers
                1..349
                    /organism="Homo sapiens"
                    /clone="126313"
                    /note="human"
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Query Match 4.7%; Score 68; DB 35; Length 349;
Best Local Similarity 64.5%; Pred. No. 9.09e-92;
Matches 151; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Db	5	ggcaacggcctgtgatctgggtggctgattccggatgacacacacagtcaccacatc	64
Qy	118	GCCAATGGCGTGGTGGCTGGCTGGAGATGCAGCGGACACTGAACACAATT	177
Db	65	agttacctgaacctggcctggctgactctctgtttcacctccactttgccattctcatg	124
Qy	178	TGGTTCTCCACCTCACCTGGCGGACACTCTCTGTGCTGCTCTCTGCGCTTCGTGCTG	237
Db	125	gtcaggaagccatgggagacactggcctctcgctgtgttcctgtgcaaatcgtcttt	184
Qy	238	GCTCACTTGGCTCTCCAGGGGACAGTGGCCCTACGGCAGGTTCTTATGCAAGCTCATCCOC	297
Db	185	accatagtggacatcaactgttgaggaaagtgttctctgatcgccctcaattgc	238
Qy	298	TCCATATGTGCTTCAACATGTTTGGCAGTGTCTTCTCGTTACTGCCATATAGC	351

RESULT	9
LOCUS	R15256
DEFINITION	yf9d03.r1 Homo sapiens cDNA clone 29866 5' similar to gb:M6749 G PROTEIN-COUPLED RECEPTOR RDC1 HOMOLOG (HUMAN);.
ACCESSION	R15256
KEYWORDS	EST.
	EST 13-APR-1995

SOURCE human clone=29866 library=Soares infant brain 1N1B vector=Lafmid BA host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Hind III Whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-AACTGCAAGATTCGGCGCCGACGAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 466)

AUTHORS
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Treviski, E., Waterston, R., Williamson, A., Wohltmann, P. and
 Zerk, D.

TITLE	JOURNAL	COMMENT
The WashU-Merck EST Project	Unpublished (1995)	

GDB: G00-402-213
Contact: Wilson RK
WashtU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 303
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 769529	Location/Qualifiers
1..466	/organism="Homo sapiens"
	/clone="29866"
	/note="human"
BASE COUNT	94 a 141 c 109 g 119 t 3 others
ORIGIN	
Query Match	2.1%; Score 31; DB 38; Length 466;
Best Local Similarity	65.0%; Pred. No. 8.03e-18;
Matches	67; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db	144	cagtggcccatggggagctcaagtgcacacacatcattcttctccatacaactc	203
QY	259	cagtggccctacggcaggttcctatgcaagctcatccctgcattgtctcaacatg	318
Db	204	ttcggcagcatttctcctcacgtgcattgagctggaacctg	246
QY	319	tttggcagtgcttctccttactgcattgacctggaatgcgt	361

RESULT 10

LOCUS R81583 183 bp mRNA EST 12-JUN-1995
YJ04b04.r1 Homo sapiens cDNA clone 147727 5' similar to gb:L25119
MU-TYPE OPIOID RECEPTOR (HUMAN);.

ACCESSION R81583

KEYWORDS EST.

SOURCE human clone=147727 library=Soares placenta Nb2HP vector=p7T73D (Pharmacla) with a modified polylinker host=DR10B (ampicillin resistant) primer=M13R1 Rsite=Not I Rsite=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

AACTGGAAGATTCCGGCCGACGAAATTTTTTTTTTTTTTTT 3'}, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 183)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1

Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.

NCBI gi: 858186

FEATURES Location/Qualifiers

source 1..183
/organism="Homo sapiens"
/clone="147727"

/note="human"

BASE COUNT 31 a 56 c 40 g 46 t 10 others

ORIGIN

Query Match 1.9%; Score 27; DB 56; Length 183;
Best Local Similarity 72.7%; Pred. No. 2.31e-11;
Matches 40; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 129 gactggctcgttagtngtcgacnattcgtctgctgacccattccat 183

||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Qy 1130 GAGTGGCGGTGGTGGTGGCTGCTTTCTGCTGCTGACTCCATACCACAT 1184

RESULT 11

LOCUS M78084 238 bp mRNA EST 26-MAY-1992

DEFINITION EST01672 Homo sapiens cDNA clone HPCPD60 similar to N-formylpeptide

receptor.

ACCESSION M78084

KEYWORDS EST.

SOURCE

human clone=HPCPD60 library=Subtracted Hippocampus, Stratagene (cat. #936205) vector=lamdaZAP-II primer=M13 Forward The hippocampus library (#4 above) was subtracted with a fibroblast cell line cDNA library (Stratagene cat. #936209; W138 lung fibroblast cell line; oligo-dT + random primed cDNA synthesis; lamdaZAP-II vector, 1.0kb average insert size.) by the method of Sive & St. John (Nucl. Acids Res. 16:10937, 1988).

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 238)

AUTHORS Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M., Uterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.

TITLE Sequence identification of 2,375 human brain genes

JOURNAL Nature 355 (6361), 632-634 (1992)

MEDLINE 92168112

COMMENT

Contact: Kerlavage AR

The Institute for Genomic Research

932 Clopper Road, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org.

NCBI gi: 273821

FEATURES Location/Qualifiers

source 1..238

/organism="Homo sapiens"

/clone="HPCPD60"

/note="human"

<1..>238

/gene="D0S1083E"

BASE COUNT 53 a 70 c 58 g 56 t 1 others

ORIGIN

Query Match 1.9%; Score 28; DB 32; Length 238;
Best Local Similarity 67.5%; Pred. No. 6.32e-13;
Matches 54; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 151 acctttgtctcgtgggtcctgggaacgggttctgtatctggctggattccggtg 210

||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Qy 97 ACTTTTTTACTGGCATTTGCCAGGCAATGGCGTGTGCTGTGGCTGGCCTGAAGATG 156

Db 211 acacacacagtcaccaccat 230

| ||||| | ||| ||

Qy 157 CAGCGGACAGTGAACACAT 176

RESULT 12

LOCUS T90501 497 bp mRNA EST 20-MAR-1995

DEFINITION yel5a04.s1 Homo sapiens cDNA clone 117822 3' similar to gb:M60626 FMET-LEU-PHE RECEPTOR (HUMAN);.

ACCESSION T90501

KEYWORDS EST.

SOURCE human clone=117822 library=Stratagene lung (#937210)

vector=pBluescript SK- host=SOIR cells (kanamycin resistant) primers=21ml3 Rsite=EcoRI Rsite2=XhoI Normal lung tissue from a 72 year old male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:

5'-GAATTCGCACGAG-3'; 3' adaptor sequence:

5'-CTCGAGTTTTTTTTTTTTTTT-3'.

ORGANISM

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 497)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

TITLE

WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 362

Source: IMAGE Consortium, LINL

This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 719014

Location/Qualifiers

1..497

FEATURES

source

/organism="Homo sapiens"

/clone="117822"

/note="human"

BASE COUNT

119 a 118 c 136 g 120 t 4 others

ORIGIN

Query Match 1..8%; Score 26; DB 86; Length 497;

Best Local Similarity 61.9%; Pred. No. 7.70e-10;

Matches 65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Db 183 tctcgttcaggccctctcaagctggcgggaaggcgtggatcagctctcccggaag 242

||||| ||||| ||||| || ||||| || ||||| || ||||| ||

Cp 1382 TCCTCACTGAAGGCTGCCTCCAGAAATTCCTGAATGGACTGCCTTCTTCTCTTAAA 1323

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 243 tctggcccatgaagacatagacatgggttgaggcagctnttg 287

|| ||||| || ||||| || ||||| || ||||| || ||||| ||

Cp 1322 TCTTCCCAGAGGCGATTAAGGAGGATTAACCACTATTG 1278

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13

LOCUS

H29103 249 bp mRNA EST 17-JUL-1995

Ym31f07.r1 Homo sapiens cDNA clone 49725 5' similar to gb:L06797

PROBABLE G PROTEIN-COUPLED RECEPTOR LCRI HOMOLOG (HUMAN);.

ACCESSION

H29103

KEYWORDS

EST.

SOURCE

human clone=49725 library=Soares infant brain INTB vector=Lafmid BA

host=DHI0B (ampicillin resistant) primer=M13R1 Rsite=Not I

Rsite2=Hind III Whole brain from a 73 days post natal female. 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

AACTGACAAATTCGGCGCCGAGCAATTTTTTTTTTTT 3']; double-stranded

cDNA was ligated to Hind III adaptors (Pharmacia), digested with

Not I and directionally cloned into the Not I and Hind III sites of

the Lafmid BA vector. Library went through one round of

normalization. Library constructed by Bento Soares and M.Fatima

Bonaldo.

Homo sapiens

ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 249)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

GDB: G00-422-535

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 198

Source: IMAGE Consortium, LINL

This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 900013

Location/Qualifiers

1..249

FEATURES

source

/organism="Homo sapiens"

/clone="49725"

/note="human"

BASE COUNT

58 a 75 c 55 g 56 t 5 others

ORIGIN

Query Match 1.7%; Score 24; DB 12; Length 249;

Best Local Similarity 60.4%; Pred. No. 6.35e-07;

Matches 64; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Db 104 ggaactgtgaacttgaactctctatgcaggcagtcctatctacacagtcacac 163

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 256 GCACGTGCCCTACGGCAGGTCTCTATGCAGCTCATCCCTCCATCATTTGCTC 315

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 164 ctctacagcagtgctctcatcctcgcttcacagtcgagcagcgt 209

|| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 316 ATGTTGGCAGTGTCTTCTGCTTACTGCGATTAGCTGGATCGCT 361

|| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14

LOCUS

H14008 198 bp DNA EST 03-JUL-1995

DEFINITION EST00034 Homo sapiens genomic clone D2-12 5'.

ACCESSION

H14008

KEYWORDS

EST.

SOURCE

Human clones=D2-12 library=Chromosome 19p12-p13.1 exon vector=pAMP10 host=E. coli DH5a primer=SD2 : 5' ATC TCA GTG GTA TTT GTC AGC 3' Exons were isolated from human chromosome 19p12-p13.1 specific cosmids from Lawrence Livermore National Laboratory using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88: 4005-4009, 1991). Amplified exons were cloned into pAMP10 by uracil cloning (GIBCOL BRL).

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 198)

Li, Q.Y.

Unpublished (1995)

COMMENT

Map: Chromosome19p12-p13.1

Contact: Li QY

Human Molecular Genetics

Queen's Medical Centre

Nottingham, NG7 2UH, UK

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Email: pdzcy1@pdnl.gene.nottingham.ac.uk.

NCBI gi: 888017

Location/Qualifiers

1..198

/organism="Homo sapiens"

/clone="D2-12"

/note="Human"

<1..>198

/map="19p12-p13.1"

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BASE COUNT

ORIGIN

Query Match

Best Local Similarity 1.6%; Score 23; DB 7; Length 198;

Matches 34; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 33 tgcaccttctcgccaccagccacagccagcctctgcaggcc 77

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 158 TGCATCTTCAGCGCCACCCACACAGCCAGCCATTCGCTGGC 114

RESULT 15

LOCUS H14012

DEFINITION EST00038 Homo sapiens genomic clone D2-32 5'.

ACCESSION H14012

KEYWORDS EST.

SOURCE Human clone=D2-32 library=Chromosome 19p12-p13.1 exon vector=pAMP10

host=E. coli DH5a primer=SD2 : 5' ATC TCA GTG GTA TTT GTC AGC 3'

Exons were isolated from human chromosome 19p12-p13.1 specific

cosmids from Lawrence Livermore National Laboratory using a

modification of the method of exon amplification (Proc. Natl.

Acad. Sci. USA 88: 4005-4009, 1991). Amplified exons were cloned

into pAMP10 by uracil cloning (GIBCO BRL).

ORGANISM Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 205)

Li, Q.Y.

Unpublished (1995)

COMMENT

Map: Chromosome19p12-p13.1

Contact: Li QY

Human Molecular Genetics

Queen's Medical Centre

Nottingham, NG7 2UH, UK

Tel: 1159249924

Fax: 1159709906

Email: pdzcy1@pdnl.gene.nottingham.ac.uk.

NCBI gi: 888021

Location/Qualifiers

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/clone="D2-32"

/note="Human"

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BASE COUNT

ORIGIN

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Matches 34; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 33 tgcaccttctcgccaccagccacagccagcctctgcaggcc 77

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Cp 158 TGCATCTTCAGCGCCACCCACACAGCCAGCCATTCGCTGGC 114

Search completed: Wed May 1 16:48:31 1996

Job time : 607 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Wed May 1 16:20:37 1996; MasPar time 896.41 Seconds
Tabular output not generated.
1142.027 Million cell updates/sec

Title: >US-08-462-355-1
Description: (1-1446) from US08462355.seq
Perfect Score: 1446
N.A. Sequence: 1 ATGCGGCTTTCTCTGCTGA.....AAGAAATAGTACACTGGTG 1446
Comp: TACCGCAGAAAGAGACGACT.....TTTCTTATCATGTTGACAC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 264399 seqs, 353985056 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-new11

1: BCT 2: FUN 3: INV1 4: INV2 5: INV3 6: MAM 7: ORG 8: PLN
9: PRI1 10: PRI2 11: PRI3 12: PRO1 13: PRO2 14: ROD 15: SYN
16: UNC 17: VRT 18: VIR

Database: genbank91

19: BCT1 20: BCT2 21: BCT3 22: BCT4 23: BCT5 24: BCT6 25: BCT7
26: INV1 27: INV2 28: INV3 29: INV4 30: INV5 31: MAM1 32: MAM2
33: PAT1 34: PAT2 35: PAT3 36: PHG 37: PLN1 38: PLN2 39: PLN3
40: PLN4 41: PLN5 42: PLN6 43: PLN7 44: PRI1 45: PRI2 46: PRI3
47: PRI4 48: PRI5 49: PRI6 50: PRI7 51: PRI8 52: PRI9 53: ROD1
54: ROD2 55: ROD3 56: ROD4 57: ROD5 58: ROD6 59: ROD7 60: STR
61: SYN 62: UNA 63: VRL1 64: VRL2 65: VRL3 66: VRL4 67: VRL5
68: VRL6 69: VRT1 70: VRT2 71: VRT3

Database: genbank-new11

72: BCT1 73: BCT2 74: INV1 75: INV2 76: MAM 77: PHG 78: PLN
79: PRI1 80: PRI2 81: PRI3 82: ROD 83: STR 84: SYN 85: UNA
86: VRL 87: VRT
88: part1

Database: u-embl44 91

Statistics: Mean 11.585; Variance 3.952; scale 2.932

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	91	6.3	1080	44	HSC5ANAPL	H.sapiens RNA for rec	1.02e-67
2	91	6.3	1092	44	HSC5AR	H.sapiens C5ar rRNA f	1.02e-67
3	91	6.3	2328	48	HUMC5AAR	Human C5a anaphylatox	1.02e-67
4	89	6.2	1050	51	HUMNEPR	Human N-formylpeptide	1.73e-65
5	89	6.2	1281	49	HUMFMPLP26	Human N-formylpeptide	1.73e-65
6	89	6.2	1866	49	HUMFMPLP	Human N-formylpeptide	1.73e-65
7	89	6.2	6931	49	HUMFPR1A	Human N-formyl peptid	1.73e-65
8	88	6.1	1268	32	RABFPR	Oryctolagus cuniculus	2.24e-64
9	86	5.9	1993	31	CFCOMC5AM	C.familiaris mRNA for	3.71e-62
10	84	5.8	1058	49	HUMFMPLPX	Human FMLP-related re	6.03e-60
11	84	5.8	1650	51	HUMFPR2A	Human formyl peptide	6.03e-60
12	84	5.8	1776	45	HSFPRHO	H.sapiens mRNA for fo	6.03e-60
13	84	5.8	1910	50	HUMHM63	Human mRNA for FMLP-r	6.03e-60
14	84	5.8	2631	49	HUMFPR1IA	Human formyl peptide	6.03e-60
15	76	5.3	1109	49	HUMFPR12	Human N-formyl recept	3.47e-51
16	75	5.2	1198	59	S50577S2	C5a anaphylatoxin rec	4.22e-50
17	75	5.2	1213	55	MUSC5ACPR	Mus musculus G protei	4.22e-50
18	72	5.0	1062	49	HUMFMPLPY	Human RMLP-related re	7.30e-47
19	73	5.0	1524	57	MUSNFORREC	Mouse N-formyl peptid	6.12e-48
20	64	4.4	1167	59	S74702	GPRI=G protein-couple	2.36e-38
21	58	4.0	1438	47	HSU13666	Human G protein-coupl	4.10e-32
22	47	3.3	1080	49	HUMCR	Homo sapiens chemoatt	4.29e-21
23	40	2.8	1583	47	HSU03642	Human G protein-coupl	1.82e-14
24	38	2.6	2051	31	CFGPCR1	Canis familiaris RDC1	1.20e-12
25	38	2.6	2097	10	HS334481	Human putative G-prot	1.20e-12
26	38	2.6	2097	47	HSU33448	Human putative G-prot	1.20e-12
27	36	2.5	3219	59	RRVTIAIIR	R.rattus mRNA for vas	7.29e-11
28	36	2.5	3295	57	RATAT1B	Rat angiotensin recep	7.29e-11
29	34	2.4	720	59	S77863	mu-opioid receptor MO	4.00e-09
30	35	2.4	1688	59	S37491	angiotensin II recept	5.47e-10
31	33	2.3	1154	47	HSU17298	Human kappa opioid re	2.85e-08
32	33	2.3	1596	9	HS224911	Human G protein-coupl	2.85e-08
33	33	2.3	1596	47	HSU22491	Human G protein-coupl	2.85e-08
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37	32	2.2	1473	47	HSU12569	Human mu opioid recep	1.97e-07
38	32	2.2	1586	58	RATMORA	Rattus norvegicus mu	1.97e-07
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40	32	2.2	1610	14	MMU26915	Mus musculus mu opioi	1.97e-07
41	32	2.2	2025	47	HSU07225	Human P2U nucleotide	1.97e-07
42	32	2.2	2025	9	HS07225	Human P2U nucleotide	1.97e-07
43	32	2.2	2135	58	RATMOR1A	Rattus norvegicus Mu	1.97e-07
44	32	2.2	2162	51	HUMMOR1X	Human Mu opiate recep	1.97e-07
45	32	2.2	2397	58	RATRORB	Rat mRNA for rat opio	1.97e-07

ALIGNMENTS

RESULT 1
LOCUS HSC5ANAPL 1080 bp DNA PRI 02-JUN-1992
DEFINITION H.sapiens RNA for receptor for C5a anaphylatoxin.
ACCESSION X58674
KEYWORDS C5a anaphylatoxin receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;

Catarrhini; Hominidae; Homo.

Ov 424 A'

Ov 424 A'

[illegible]

RESULT	5				
LOCUS	HUMFMLP26	1281 bp	mRNA	PRI	23-JAN-1991
DEFINITION	Human N-formylpeptide receptor (fMLP-R26) mRNA, complete cds.				
ACCESSION	M60627	M33538			
KEYWORDS	N-formyl peptide receptor; N-formylpeptide receptor fMLP-R26.				
SOURCE	Human, cDNA to mRNA.				

REFERENCE
AUTHORS
TITLE

Eukaryotes; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea. 1 (bases 1 to 1281)

Bouley, F., Tardif, M., Brouchon, L. and Vignaie, P.
The human N-formylpeptide receptor. Characterization of two cDNA isolates and evidence for a new subfamily of G-protein-coupled receptors

receptors

JOURNAL Biochemistry 29, 11123-11133 (1990)

COMMENT MEDLINE 91105045

NCBI gi: 182664

Location/Qualifiers

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/sequenced_mol="cDNA to mRNA"

<1..1281

62..1114

/note="NCBI gi: 182665"

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LIIRVTPGCKGTWACTFNSFWNDPKERINVAVMLTVRGIRFIIGFSAPMSIVA
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285 a 353 c 313 g 330 t

BASE COUNT

ORIGIN

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Best Local Similarity 63.9%; Pred. No. 1.73e-65;
Matches 205; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

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157	Qy	CAGCGGACAGTGAACACAAATTTGGTTCTCCACCTCACCTTTGGGGACCTCTCTGTGCTGC	216
287	Db	teocattttgcatattcttcattgctcaggaagccatggagacattggctcttcgctgg	346
217	Qy	CTCTCTTGGCCTTCTCGCTGGCTACTTGGGCTTCCAGGGACAGTGGCCCTACGGCAGG	276
347	Db	ttctcttgcaaaattcgctctttaccatagtcagacatacaetgttcgggaagtgtcttcctg	406
277	Qy	TTCTCATTGAAGAGTCATCCCTTCCAATGTTTGTCTCAACATGTTTGGCAGTGTCTTCTG	336
407	Db	atcgccctcatigtctcggaccgctgtgttgctgcctccatccagctcggaccacaac	466
337	Qy	CTTACTGCCAATTAGCCTGGATCGCTGTCTTGTGGTATTCAAGCCAATCTGGTGTCAGAAT	396
467	Db	caccgcacgtgagcctggcc	487
397	Qy	CATCGCAATGTAGGGATGGCC	417

6					PRI	23-JAN-1991
RESULT	HUMFMLP	1866 bp	mRNA			
LOCUS	DEFINITION	Human N-formylpeptide receptor	(fMLP-R98) mRNA,	complete cds.		
ACCESSION	M60626	M33537				
KEYWORDS	N-formyl peptide receptor;	N-formylpeptide receptor fMLP-R98.				
SOURCE	Human, cDNA to mRNA.					

ORGANISM Homo sapiens

REFERENCE Boulay, F., Tardif, M., Bouchon, L. and Vignais, P. 1 (bases 1 to 1866)

AUTHORS Boulay, F., Tardif, M., Bouchon, L. and Vignais, P.

TITLE The human N-formylpeptide receptor. Characterization of two cDNA isolates and evidence for a new subfamily of G-protein-coupled receptors

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JOURNAL Biochemistry 29, 11123-11133 (1990)
MEDLINE 91105045
COMMENT NCBI gi: 182662
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ORIGIN

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Best Local Similarity 63.9%; Pred. No. 1.73e-65;

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Qy	157	CACGGGACAGTGACACAAATTTGGTCTCTCACCTCACCTTGGCGGACCTCTCTGCTGC	216							
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Db	451	cacgcacagtgcagctggcc	471							
Qy	397	CATCGCAATGTAGGATGGCC	417							

RESULT	7	
LOCUS	HUMFPR1A	6931 bp DNA PRI 18-MAR-1994
DEFINITION	Human N-formyl peptide receptor (FPR1) gene, complete cds and Alu repeats.	
ACCESSION	L10820	
KEYWORDS	G protein; G protein coupled receptor; N-formyl peptide; N-formyl peptide receptor; formyl peptide receptor; peptide receptor; pertussis toxin; phagocytosis; plasma membrane; transmembrane domain; transmembrane receptor.	
SOURCE	Homo sapiens (Library: Lambda FIX) DNA.	
ORGANISM	Homo sapiens	
REFERENCE	1 (sites)	
AUTHORS	Boulay,F., Tardif,M., Brouchon,L. and Vignais,P.	
TITLE	The human N-formylpeptide receptor. Characterization of two cDNA isolates and evidence for a new subfamily of G-Protein-Coupled receptors	
JOURNAL	Biochemistry 29, 11123-11133 (1990)	
MEDLINE	91105045	
REFERENCE	2 (sites)	
AUTHORS	Perez,H.D.	
TITLE	Cloning of the gene coding for a human receptor for formylpeptides	
JOURNAL	Unpublished (1992)	
REFERENCE	3 (bases 1 to 6931)	
AUTHORS	Murphy,P.M., Tiffany,H.L., McDermott,D. and Ahuja,S.K.	
TITLE	Sequence and organization of the human N-formyl peptide receptor-encoding gene	
JOURNAL	Gene 133 (2), 285-290 (1993)	
MEDLINE	94040825	
COMMENT	NCBI gi: 182739	
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	Best Local Similarity	63.6%;	Pred. No. 1.73e-65;		
	Matches	205;	Conservative	0;	Mismatches 116; Indels 0; Gaps 0;
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Qy	157	CAGCGGACAGTAGACAAATTTGGTTCTCTCCACCTCACTTCCTGGCGGACCTCTCTCTGCTGC	216		
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3' UTR

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Best Local Similarity 62.1%; Pred. No. 6.03e-60;
Matches 216; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

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Qy 70 ATTCTCTCCATGCTCATCTCAGCCTTACTTTTTTACTGGGATTGCCAGCAATGGCGTG 129

Db 178 gtgctcgtggtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgtggtc 237
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Db 238 ctggcctcgtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgtg 297
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Qy 190 CTCACCTTGGCGGACCTCCTCTGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 249

Db 298 atgggagaaaaatggccttttggctggttcctggtggtggtggtggtggtggtggtggt 357
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Qy 250 CTCACGACAGTGGCGCTACGCGGAGGTTCTATGCAAGCTCATCCCTCCATCATGCTC 309

Db 358 atcaacctctttggaagtgtctcttctggtggtggtggtggtggtggtggtggtggtggt 417
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Qy 310 CTCACATGTTTGGCAGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 369

Db 418 gtctgcatcgaagtctgggcccagaaccacgcgaactgtgagctgagctgagctgagctg 465
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 370 GTATTCAAGCAATCTGGTGTGAGATCATCGCAATCATCGCAATGATAGGATGGCC 417
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RESULT 12
LOCUS HSEPRHO 1776 bp RNA PRI 05-JUN-1992
DEFINITION H.sapiens mRNA for formyl peptide receptor 70% homologue.
ACCESSION X63819
KEYWORDS formyl peptide receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Cathartini; Hominidae; Homo.
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REFERENCE 1 (bases 1 to 1770)
AUTHORS Perez, H.D.
TITLE Cloning of an orphan receptor related to the formyl peptide
receptor of human neutrophils
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1776)
AUTHORS Perez, D.H.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-1992) to the EMBL/GenBank/DBJ databases. D.H.
Perez, Berlex Biosciences, 213 E. Grand Ave, South San Francisco,
CA 94080, USA
NCBI gi: 31460
FEATURES
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1..1776
Location/Qualifiers
/organism="Homo sapiens"
/tissue_type="bone marrow"
/cell_type="neutrophils"
/clone_lib="human bone marrow"
/clone="pINF2"
/sex="Male"
154..1209
/note="NCBI gi: 31461"
/codon_start=1
/product="formyl peptide receptor 70% homologue"
/translation="METNFTPLNEYEVSYESAGYTVLRILPLVLGVTFVLGVGN
GLVHWAGFRMTRVTTCYINLALADSFATLPFLIVSMAMGEKPFGEFLCKLIH
IYVDINLGSVFLIGTICVLPVWQNRHTVSLAMKRVIVGFWILALVLTLPV
FLFTVTPNGDTCYTFNFASGSGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVA
ICYGLIAKHKKMIKSSRPLRVLTAVASFFICWPFQVALLGTVWIKEMLFYCK
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CDS
BASE COUNT 421 a 400 c 400 g 550 t 5 others
ORIGIN
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Best Local Similarity 62.1%; Pred. No. 6.03e-60;
Matches 216; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Db 232 atctcccatggtggtcgttggtggtcacccttgcctcggtggtcctgggaatggcctt 291
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Qy 70 ATTCTCTCCATGCTCATCTCAGCCTTACTTTTTTACTGGGATTGCCAGCAATGGCGTG 129

Db 292 gtgctcgtggtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgt 351
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Qy 130 GTCTGTGGTGGCTGGCTGAGATGACGCGGACAGTGAACAAATTTGGTTCTCCAC 189

Db 352 ctggcctcgtggtcgttcttcttcacggccacattaccattcctcattgtccatggcc 411
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 190 CTCACCTTGGCGGACCTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 249

Db 412 atgggagaaaaatggccttttggctggttcctgtggtggtggtggtggtggtggtggtg 471
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Qy 250 CTCACGACAGTGGCGCTACGCGGAGGTTCTCTATGCAAGCTCATCCCTCCATCATGCTC 309

Db 472 atcaacctctttggaagtgtctcttctgattggtttcattgcaactggaactgcaattgt 531
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Qy 310 CTCACATGTTTGGCAGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 369

Db 532 gtccctgcatcgaagtctgggcccagaaccacgcgaactgtgagctgagctgagctgagcc 579
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Qy 370 GTATTCAAGCAATCTGGTGTGAGATCATCGCAATCATCGCAATGATAGGATGGCC 417
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RESULT 13

17-FEB-1994

NCBI ai: 219864

length 1910:

172

- tarctaac 232

Interference 292

352

TCA TTGTC 309

malia: Theria:

2. COMMITMENT

2210423
CBI ci: 182741

CDS

polyA site

Length 2631:

contact 910

Dbb

162 tctcattgttagtccaggagtcacacctttgtctcggggctctggccaatgggttgtga 221
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Qy 74 TCTCCATGGTCATTCTCAGCCTTACTTTTTTACTTGGGATGCCAGGCATGGCGTGCTC 133
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Dbb

222 tctgggtggctggattccgggatcacacgcacagtcacaaccactctgttaacctgaacctgg 281
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Qy 134 TGTGGGTGGCTGGCGCTGAAGATGACGGCAGATGAACAATAATTGGTTCTCCACCTCA 193
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Dbb

282 ccctaagtcaactctctttcaagtgcatactaccattccagaatggctcagtcgcccatga 341
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Qy 194 CTTTGGCGAACCCTCCTGCTGCCTCTCGTTGGCTTTCGCTGGGCTCACATTGGCTCTCC 253
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Dbb

342 gagaaatatggcctbtlttggtcattcctctatgtaagttagtctaatgttatgatagacatca 401
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Qy 254 AGGCACAGTGGCCCTTAGCGGAGGTTCCTATGCANAGCTCATCCCTCCCATCATTTGCTCTCA 313
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Dbb

402 acctgtttgtcagtgctacctgatcaccatactgtctggacgcgtgtatttgtctcc 461
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Qy 314 ACATGTTTGGCAGTGCTTCCTCTGCTTAAGTGCCATTAGCCTGTGATCGCTGTCTTGTGTAT 373
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Qy 374 TCAGCCCAATCTGGTGTGAGAAATCATGGCA 403

Search completed: Wed May 1 16:35:48 1996

Job time : 911 secs.

(TM)

Result No.	Query		DB	ID	Description	Pred. No.	
	Score	Match Length					
c 1	85	5.9	1047	2	Q10572	Human Natriuretic Pep	1.63e-39
c 2	62	4.3	1047	2	Q10572	Human Natriuretic Pep	5.41e-24
c 3	47	3.3	204	1	N81164	Base substituted E.co	2.42e-14
c 4	43	3.0	91	9	Q51746	Oligonucleotide probe	7.19e-12
c 5	42	2.9	91	9	Q51746	Oligonucleotide probe	2.93e-11
c 6	41	2.8	204	1	N81164	Base substituted E.co	1.18e-10
c 7	40	2.8	1872	11	Q66176	Seven transmembrane r	4.74e-10
c 8	38	2.6	2098	11	Q66177	Seven transmembrane r	7.38e-09
c 9	34	2.4	112	12	Q70469	Generic DNA sequence	1.57e-06

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FT Modified -site 195..197
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FT Modified -site 244..246
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FT Modified -site 277..279
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FT Modified -site 349..351
FT /label= N-glycos site
FT Modified -site 600..602
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PN W09100292-A.
PD 10-JAN-1991.
PF 22-JUN-1990; 003586.
PR 23-JUN-1989; US-370673.
PA (GETH ) GENENTECH INC.
PI Chang M, Goeddel D, Lowe D;
DR WPI; 91-036711/05.
DR N-PSDB; Q10324.
PT Natriuretic protein receptor B - for diagnosis and treatment of
PT kidney failure, heart failure, hyperaldosteronism, glaucoma etc.
PS Claim 3; Fig 1; 49pp; English.
CC The sequence was derived from the DNA encoding natriuretic peptide
CC receptor B, NPRB, having guanyl cyclase (GC) activity and protein
CC kinase activity. The DNA can be inserted into expression vectors
CC for the prodn. of the protein, opt. after being mutated to produce
CC NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=
CC 114,952). The protein (or variants) can be used in treatment of
CC natriuretic peptide disorders, and also to isolate peptides using
CC affinity chromatography. Antibodies with affinity for NPRB can
CC also be prepd.
SQ Sequence 1047 BP; 87 A; 15 C; 83 G; 51 T;

Query Match 5.9%; Score 85; DB 2; Length 1047;
Best Local Similarity 9.0%; Pred. No. 1.63e-39;
Matches 88; Conservative 279; Mismatches 597; Indels 12; Gaps 12;

Db 29 vnnnnhnsyavawrvgnavanavangrannvdrnrvssnnngacsnynannsaavdnk 88
Cp 1228 CCAGGGAGTTTCTGGTCAAGCAATGACAGGACTCCCAAAATGTGTATGAGATCC 1169

Db 89 nyhdndnnngcvynaaavarnashwrnmntagavaasgnakndhyrtnvrtgnsank 148
Cp 1168 AGCAGACAGAAAGACAGCCACCACCCAGCGGCTCGAAAGGTTTGTCTGAGACT 1109

Db 149 ngnnvvtthghnnwtarannnyndatddrhyntnngvnnannsgnsvnhvnyarnng 208
Cp 1108 TGGCGACGGCCCTTTCAT-TCGGAGAGCAATGAAGCTGTAAAGGCTATATGATA 1050

Db 209 gnnnathnrangrnrvncggnnmhnnhnnnannrnnntngdyvnnndvngnsragnt 268
Cp 1049 ACAGAGGCGAGAGGAACCCACACCTAGCTGTATGCTGTAT-T-CCACAGGGGTG 992

Db 269 atgrwdrntrnnanrananntvntyrnnnnnnnnnnnnnnnnnnrnnrnnrnnrnnng 328
Cp 991 TTGGCACTTGATCGTCACTGTGAATTGGCGCTAAATTTGTAATTCCTGGAACCTTGTG 932

Db 329 nannnagcnydgpnnyavvnnntnnngtrndgrnrvnkngrryhgvtgngvmdkndr 388
Cp 931 GTAGCT-CAGACTCGTAGAGGAATTCGTAGAAGCGCTAGGGAACAGCTTTAAATGATGA 873

Db 389 ntshvnmangdnsgdnnaahysganknwrtgrnnnwkvgnnsdnnncandndhsc 448
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Cp 872 GAGAGAAAGCATCAGAGTTATCC-AGTGGCTGGTTTCGTGATCTTCAATAGGAACCC 814
Db 449 dktntethav-angtntnnmgvsennnrkmmnknmmnnrnrwnnnnnngsnry 507
Cp 813 ACTGGGGATTTTAGTGCAGACCACATCAGCAGGTTTAAATACATTAGATACA-GATT-T 756
Db 508 hkgagrsntnsrgssygsmtahgkynnmantghnkgnvvvankhvnkrntntrvnnn 567
Cp 755 TGACTTTGTTAACTTAGCAGAACCCCTAGGAGTGAATCTGCA-GAAGGTCTTTGAATGT 697
Db 568 nkhrdvnnhntnmgacndnnnncvntnycnrgsnndnnnndsnndnnmtrvnnndn 627
Cp 696 TTGAGGTTGGAAGACAGCTGGGAGCTGTCAGAGCATCATTTGTTGGAAAGAGGAAGG 637
Db 628 vkmmnnhnsnshgnsksncvvdvsnrvnknktdygnasnrstannndnnnyaknnt 687
Cp 636 ATCTAACCTATCATTTCTCCAGCGGCTGAACAATGTTTCAAGAGACCTGTTTTC 577
Db 688 annnnegnnnttgmnaadvysngnnnnnnnanzngvnnngndnsknknvkvngnry 747
Cp 576 TAGTGGATCCCATAAAGTCTGGATAATCTAATGAGCTGAGAGACCAAAATTTGTAGCC 517
Db 748 nrnsndrtnnnnnnvnmnrwandrndngnknknrrnknngtstendnnnnrnn 807
Cp 516 ACATCTATTAGTGTCTGTAGTCAAGATTTCCGGTACAGACACAGGAAATGCACAA 457
Db 808 yannnnkvnnrtnaynnnkrkanannynnnhsvannnkrntvmanandvtnynsdn 867
Cp 456 CACAAA-AGCCACCCACCCAGATACATCCACAGATAGACAGGCCATCCCTACATTCGAT 398
Db 868 vntansanstmmvvtvnnndnytcndannndndvykvtntngdaymvvsgnngnngriha 927
Cp 397 GATTCTGA-CACAGATTTGGCTTGAATACCAAGACAGCGCATCCAGGCTAATGGCAGTA 339

Db 928 nnarmanandvsnrnrhndnnrnnrghvntgncvavngvknrvnnngdvtnta 987
Cp 338 AGCAGGAAGACACTGCCAAACATGTTGAGGACAATG-ATGGAGGGGATGAGCTTGCATAG 280

Db 988 srmsngnankhves 1003
Cp 279 GAACCTCCCTAGGCGC 264

RESULT 2
ID Q10572 standard; DNA; 1047 BP.
AC Q10572;
DT 09-APR-1991 (first entry)
DE Human Natriuretic Peptide Receptor B.
KW NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
KW hyperaldosteronism; glaucoma; guanyl cyclase.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= signal sequence
FT Protein 12
FT /label= mature NPRB
FT Domain 23..455
FT /label= extracellular domain
FT /note= "binds natriuretic peptides A, B and C"
FT Domain 456..456
FT /label= transmembrane domain
FT Domain 479..1047
FT /label= cytoplasmic domain
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CC generic sequences are shown in Q70465-68. Other specific peptides
CC generated by these generic sequences are shown in R65150-54. TSARs are
CC concatenated heterofunctional proteins or peptides, comprising at least
CC two functional regions - a binding domain with affinity for a ligand and
CC a second effector peptide portion that is chemically or biologically
CC active. They may further comprise a linker peptide between the 2 domains.
CC The oligonucleotides are also designed so that the expressed peptide
CC contains 2 or 4 cysteine residues positioned in, or flanking, the
CC unpredicted or variant residues. These residues confer some degree of
CC conformational rigidity to the peptides. The TSARs or compsns. comprising
CC a TSAR binding domain can be used in vivo to deliver a chemically or
CC biologically active moiety, eg. metal ion, radioisotope, peptide, toxin
CC or enzyme, to the specific target or on the cell. They can also replace
CC the function of macromolecules, eg. monoclonal or polyclonal antibodies
CC and therefore circumvent the need for complex methods of hybridoma
CC formation or in vivo antibody production. The TSARs are easily
CC characterised and have designed activity allowing direct and rapid
CC detection in a screening process.
SQ Sequence 114 BP; 0 A; 4 C; 4 G; 4 T;

Query Match 2.4%; Score 34; DB 12; Length 114;
Best Local Similarity 6.4%; Pred. No. 1.57e-06;
Matches 7; Conservative 30; Mismatches 73; Indels 0; Gaps 0;

Db 2 gcnmbnbnbnbnbnbnbnbnbnbtgcnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn 61

Qy 146 GCGTGAAGTCAGCGGACAGTCACACAAATTTGGTCTCCACCTCAGCTGGCGGACC 205

Db 62 nbmbtgcnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn 111

Qy 206 TCCTCTGCTGCTCTCTCTGCGCTTCGCTGCTCACTTGGCTCTCCAG 255

RESULT 10

ID Q70465 standard; DNA; 114 BP.
AC Q70465;
DT 05-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc feature 55..60
FT /tag= a
FT /note= "this sequence represents '2'; 2 can be a
FT sequence of 6, 9 or 12 nucleotides (see
FT comments)"
PN W09418318-A.
PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK;
DR WPI; 94-279739/34.
DR P-PSDB; R65150 and R65151.
DR Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.
CC Q70465 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be

CC represented as follows: X(NNB)6(TCC)(NNB)14(TCC)(NNB)3Y. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC not specified further. Other generic sequences are shown in Q70466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active. They may further comprise a linker
CC peptide between the 2 domains. The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
CC in, or flanking, the unpredicted or variant residues. These residues
CC confer some degree of conformational rigidity to the peptides. The TSARs
CC or compsns. comprising a TSAR binding domain can be used in vivo to
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC cell. They can also replace the function of macromolecules, eg.
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC for complex methods of hybridoma formation or in vivo antibody
CC production. The TSARs are easily characterised and have designed
CC activity allowing direct and rapid detection in a screening process.
SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

Query Match 2.4%; Score 34; DB 12; Length 114;
Best Local Similarity 3.6%; Pred. No. 1.57e-06;
Matches 4; Conservative 33; Mismatches 75; Indels 0; Gaps 0;

Db 3 bnnbnbnbnbnbnbnbnbtgcnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn 62

Qy 120 CAATGGCGTGGTGGTGGCTGGCTGGCTGAAGATCGACGCGACGTGAACACAAATTTG 179

Db 63 bnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbtgcnnbnbnbnbn 114

Qy 180 GTTCTCCACCTCAGCTGGCGGACCTCTCTGCTGCTCTCTCTGCTGCTTC 231

RESULT 11

ID Q70470 standard; DNA; 114 BP.
AC Q70470;
DT 10-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc feature 55..60
FT /tag= a
FT /note= "encoded by Z (see comments)"
PN W09418318-A.
PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK;
DR WPI; 94-279739/34.
DR P-PSDB; R58378.
DR Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 36; 255pp; English.
CC Q70470 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be

CC represented as follows: X(NNB)16(TGC)12(NNB)16(TGC)(NNB)1Y.X

PS Disclosure; Page 35; 255pp; English.

CC Q70468 is a generic DNA sequence used to generate random TSAR (Totally

PS Disclosure; Page 35; 255pp; English.

PT Identifying proteins or pe

PT Identifying proteins or peptide(s) which bind a ligand - by

	Query Match	2.4%;	Score 34;	DB 12;	Length 114;
	Best Local Similarity	4.5%;	Pred. No. 1.57e-06;		
	Matches	5;	Conservative	32; Mismatches	75; Indels
				Gaps	0;
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Db	3	bmbnbnbnbnbnbtgcmbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnnnnnnn	62		
Cp	258	TUCCTGAGACCAACTGAGCGCAGGAAGCCAAAGCAGGCAGCACGAGGAGTCCGC	199		
<hr/>					
Db	63	bmbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn	114		
<hr/>					
Cp	198	CAAAGTGAGGTGAGAACACCAAAATTGGTTCACTGTCGCCGTGCATCTTCAGG	147		

Search completed: Wed May 1 16:38:05 1996
Job time : 118 secs.

[illegible]

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RESULT      2
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TITLE      A37963      #type complete
ORGANISM    complement C5a anaphylatoxin receptor - human
#formal name Homo sapiens #common name man
DATE        22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
            28-Oct-1994
ACCESSIONS  A37963; S13646; S30518
REFERENCE    A37963
#authors    Boulay, F.; Mery, L.; Tardif, M.; Brouchon, L.; Vignais, P.
#journal     Biochemistry (1991) 30:2993-2999
#title       Expression cloning of a receptor for C5a anaphylatoxin on
            differentiated HL-60 cells.
#cross-references MUID:91175748

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#accession A37963
#molecule_type mRNA
#residues 1-350 #label BOU
#cross-references GB:J05327

REFERENCE
#authors Gerard, N.P.; Gerard, C.
#journal Nature (1991) 349:614-617
#title The chemotactic receptor for human C5a anaphylatoxin.
#cross-references M01D:91156029
#accession SI3646

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#PROTEIN: 1 556 PROTEIN. QM
KEYWORDS G protein-coupled receptor; glycoprotein; membrane protein
FEATURE
5 #binding site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 350 #molecular-weight 39320 #checksum 3557

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Query Match 16.2%; Score 580; DB 10; Length 350;
Best Local Similarity 47.2%; Pred. No. 2.58e-70;
Matches 67; Conservative 45; Mismatches 30; Indels 0; Gaps 0

Db 36 pdilalvifavflvgvlgvalvvtafeakrtinaifwlnlavadfslclalpilfts 95

Qy 22 PVILSMVILSTFLGLPGNGLVWAGLKMQRVTNTWFLHLT*
LADLCCCLSLAFSLAH 81

Db 96 ivqhhwpggaacsilpslillnmyasilllatissadrflvlvfkpwcmfrgaglawi 155

Qy 82 LALQQWPYGRFLCKLPSIIVLNFGSVFLLTAISLDRCLVTFKPWCQNHNRVGMACS 141

Db 156 acavawglallltipsflyrvw 177

Qy 142 ICGCIWWAFVLCIPVFYREI 163

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RESULT      3
ENTRY
TITLE
ALTERNATE_NAMES  B42009      #type complete
                  FM1P-related receptor 1 - human
                  FM1P receptor homolog FPR2; formyl peptide receptor like-1;
                  probable chemotactic receptor FPRH1
ORGANISM      #formal name Homo sapiens #common name man

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DATE	30-Sep-1993	sequence_revision	14-Jul-1995	text_change
ACCESSIONS	B42009; JC1258; JQ1521; A42492; S21581			
REFERENCE	A42009			
authors	Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.			
# journal	Genomics (1992)	13:437-440		
#title	Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), and two FMLP receptor homologue orphan receptors (FPRH1, FPRH2) to chromosome 19.			

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#note
nucleotide sequence is not given; authors translated the
codons GTC for residue 15 as Glu, TCT for residue 19
as Thr, and GGC for residues 264 as Ala; translation
for residue 265 was not shown

REFERENCE	JC1258
#authors	Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Andrews, W.H.
#journal	Gene (1992) 118:303-304
#title	Cloning of a cDNA encoding a receptor related to the formyl peptide receptor of human neutrophils.
#cross-references	MUID:92380523
#accession	JC1258

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 #authors
 Ye, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.;
 Cochran, C.G.
 #journal
 Biochem. Biophys. Res. Commun. (1992) 184:582-589
 #title
 Isolation of a cDNA that encodes a novel granulocyte N-formyl
 peptide receptor.

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#cross-references MUID:92246937
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#molecule_type mRNA
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#cross-references GB:M88107
#experimental_source granulocytes
#note
formyl peptide-stimulated calcium mobilization
comparable to that of the formyl peptide receptor is
seen at 1000 times higher concentrations of ligand
fMet-Leu-Phe

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REFERENCE
#authors
#journal
#title
A42492
Murphy, P. M.; Orzelik, T.; Kenney, R. T.; Tiffany, H. L.;
McDermott, D.; Francke, U.
J. Biol. Chem. (1992) 267:7637-7643
A structural homologue of the N-formyl peptide receptor.
Characterization and chromosome mapping of a peptide
chemoattractant receptor family.

```
#cross-references MUID:92218423
#accession A42492
#molecule_type mRNA
#residues 1-351 #label MUR
#cross-references NCBI:94159; NCBI:94160
#note sequence extracted from NCBI backbone
COMMENT This G-protein coupled receptor, homologous to the N-formyl peptide
receptor FPRI, does not bind prototype N-formyl peptide ligands
(reference A42492, but see also J01521). It is expressed only on
differentiated myeloid cells and is probably a chemotactic
```


TITLE	N-formyl peptide chemotactic receptor - mouse
ORGANISM	#formal_name Mus musculus #common name house mouse
DATE	23-Mar-1995 accession_revision 23-Mar-1995 #text_change 23-Mar-1995
ACCESSIONS	A49542
REFERENCE	A49542
authors	Gao, J.L.; Murphy, P.M.
#journal	J. Biol. Chem. (1993) 268:25395-25401
#title	Species and subtype variants of the N-formyl peptide chemotactic receptor reveal multiple important functional domains.
#accession	A49542
##status	preliminary
##molecule_type	DNA
##residues	1-364 ##label GAO
##cross-references	GB:L22181
GENETICS	
#introns	
#status	absent
KEYWORDS	chemotaxis; transmembrane protein
SUMMARY	#length 364 #molecular-weight 40326 #checksum 3042
Query Match	14.9%; Score 536; DB 11; Length 364;
Best Local Similarity	43.4%; Pred. No. 3,28e+63;
Matches	75; Conservative 54; Mismatches 38; Indels 6; Gaps 6
Db	35 vfsyliavftvlgvlnglvigwagfrmkhtvtisylvnladaf-cfstlpfyasm 93
Qy	24 ILSWILSLTFLGUPNGVLVAVIGAKMQRTVTNTIMFHLTLADLCCLLS-LAFSLAHL 82
Db	94 vmgghwpfwfmcckfiyvridinlfsgvfllialaldrcicvhlhpwaqnhrtvelakvv 153
Qy	83 ALQGOMPYGRFLCKLIPISITVLNMFSGVFLLTAISLDRCIUVWFKSIWCQHRRNVGMAGSI 142
Db	154 iivpwicafltltpvil-r-l-ttvpnsrlg-pgktactdfsfptkwdpvekr 202
Qy	143 CGCIWWAFVICIPVEVREIFTDTHNRCCYKFGGLSSSDYPDFYGDPLENR 195
RESULT	7
ENTRY	A46520 #type complete
TITLE	N-formyl peptide receptor - rabbit
ORGANISM	#formal_name Oryctolagus cuniculus #common_name domestic rabbit
DATE	18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
ACCESSIONS	A46520
REFERENCE	A46520
authors	Ye, R.D.; Quehenberger, O.; Thomas, K.W.; Navarro, J.; Cavanagh, S.L.; Prossnitz, E.R.; Cochran, C.G.
#journal	J. Immunol. (1993) 150:1383-1394
#title	The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression, and structure/function implications.
#cross-references	MUID:93163563
#accession	A46520
##status	preliminary; not compared with conceptual translation
##molecule_type	nucleic acid
##residues	1-352 ##label YE1
##cross-references	NCBI:P124908
##experimental_source	NZW, neutrophils
#note	sequence extracted from NCBI backbone
SUMMARY	#length 352 #molecular-weight 38674 #checksum 7066
Query Match	14.6%; Score 525; DB 11; Length 352;
Best Local Similarity	47.3%; Pred. No. 1.92e-61;

Matches	70; Conservative	44; Mismatches	31; Indels	3; Gaps	3;
Db	27	vfsyllvltfvlgvqlngvltvqfmthtvttsivlnlalnadfsttltplffivtk	86		
Qy	24	ILSWILSLTFLGLPGNGVIMVAGIKMQRVTNTIWFILHTLADLLCLSLAFSLAHILA	83		
Db	87	lgghwpfswflekfvftivdninlfgsvflialaldrcicvlpwvqgmhrnvelakv	146		
Qy	84	LQSQMPYGRFLKTLPSIIVINFGSVFLTAISLDRCLVFKPIMQCNHRNVGMAC	143		
Db	147	vgpwicaltlpvlvii-r-v-ttlshpr	171		
Qy	144	GCIMVAVFLCIPFVYREIFTTDNHR	171		
RESULT	8				
ENTRY	A42009	#type complete			
TITLE	N-formyl peptide receptor - human				
ALTERNATE_NAMES	FMLP receptor				
ORGANISM	#formal_name Homo sapiens	#common_name man			
DATE	30-Sep-1993	#sequence_revision 14-Jul-1995	#text_change 14-Jul-1995		
ACCESSIONS	JC2014; A36309; A35495; A42009				
REFERENCE	JC2014				
#authors	Murphy, P.M.; Tiffany, H.L.; McDermott, D.; Ahuja, S.K.				
#journal	Gene (1993) 133:285-290				
#title	Sequence and organization of the human N-formyl peptide receptor-encoding gene.				
#accession	JC2014				
#molecule_type	mRNA				
#residues	1-350	#label MUR			
#cross-references	CB:L10820				
#note	192-Asn was also found				
REFERENCE	A36309				
#authors	Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P.				
#journal	Biochemistry (1990) 29:11123-11133				
#title	The human N-formylpeptide receptor. Characterization of two cDNA isolates and evidence for a new subfamily of G-protein-coupled receptors.				
#cross-references	MUID:91105045				
#accession	A36309				
#status	not compared with conceptual translation				
#molecule_type	mRNA				
#residues	1-191, 'N', 193-345, 'E', 347-350	#label BOU			
REFERENCE	A35495				
#authors	Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P.				
#journal	Biochem. Biophys. Res. Commun. (1990) 168:1103-1109				
#title	Synthesis and use of a novel N-formyl peptide derivative to isolate a human N-formyl peptide receptor cDNA.				
#cross-references	MUID:90267449				
#accession	A35495				
#molecule_type	mRNA				
#residues	1-100, 'L', 102-191, 'N', 193-350	#label BO2			
REFERENCE	A42009				
#authors	Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.				
#journal	Genomics (1992) 13:437-440				
#title	Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), and two FMLP receptor homologues orphan receptors (FPRH1, FPRH2) to chromosome 19.				
#accession	A42009				
#status	not compared with conceptual translation				
#molecule_type	DNA				
#residues	1, 'G', 3-28, 30-100, 'L', 102-104, 106-112, 'FLTA', 115-176,				

May 1 15:23

US-08-462-355-2.rpr

15

Db 86 vytameyrwpgnylckiasasvsnlyasvfltlclsidrylaivhpmksrlrrtmlva 145

[illegible]

Qy 80 AHIALQGQWPYGRFLCKLIPSIIVLMFGSVFLLTAISLDRLVLVFKPIWCQNHRNVGMA 139

Db 146 kvtciiwllaglaslpaiihrvffientnitvcafhyesqnstl 191

[illegible]

Qy 140 CSICGCIWVAVFLCIPVFVYREIFTTDNHN-R-CGYKF-GLSSSL 182

Search completed: Wed May 1 15:30:45 1996
Job time : 75 secs.

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 1 15:28:15 1996; MasPar time 9.52 Seconds
419.333 Million cell updates/sec
Tabular output not generated.

Title: >US-08-462-355-2
Description: (1-482) from US08462355.pep
Perfect Score: 3591
Sequence: 1 MASFSAEYNSTDLISQPMNE.....TRSTHCPSNNVISERNSTTV 482

Scoring table: PAM 150
Gap 11

Searched: 70887 seqs, 8282111 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq22
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14

Statistics: Mean 35.628; Variance 159.312; scale 0.224

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	390	10.9	377	10	R53751	Seven transmembrane r 7.17e-24
2	355	9.9	359	9	R44531	Human angiotensin II 9.41e-21
3	340	9.5	337	10	R53753	Seven transmembrane r 2.00e-19
4	340	9.5	352	12	R68812	Human monocyte PF4AR. 2.00e-19
5	340	9.5	352	5	R27792	New platelet factor 4 2.00e-19
6	335	9.3	355	7	R33420	Human IL-8 receptor f 5.53e-19
7	335	9.3	360	6	R28273	Sequence in a low aff 5.53e-19
8	335	9.3	1064	14	R70124	IL8-R type 2-GPB 130 5.53e-19
9	331	9.2	355	6	R28272	Sequence in a high af 1.25e-18
10	325	9.1	350	5	R27791	Interleukin-8 recepto 4.21e-18
11	325	9.1	350	12	R68811	Interleukin-8 recepto 4.21e-18
12	325	9.1	1060	14	R70123	IL8-R type 1-GPB 130 4.21e-18

13	315	8.8	418	7	R39263	Human somatostatin re 3.18e-17
14	314	8.7	380	10	R53750	Seven transmembrane r 3.89e-17
15	311	8.7	428	7	R39264	Murine somatostatin r 7.12e-17
16	308	8.6	400	14	R76780	Human mu opiate recep 1.30e-16
17	306	8.5	356	11	R65188	Murine mu-subtype opi 1.95e-16
18	305	8.5	395	13	R66920	Murine C140 receptor. 2.38e-16
19	306	8.5	398	14	R76781	Rat mu opiate recepto 1.95e-16
20	305	8.5	398	13	R71964	Rat mu opiate recepto 2.38e-16
21	305	8.5	399	13	R66922	Murine C140 receptor 2.38e-16
22	305	8.5	400	13	R71966	Human mu opiate recep 2.38e-16
23	297	8.3	333	13	R72985	Epsilon opiod recept 1.19e-15
24	296	8.2	354	11	R53932	Interleukin 8 (IL-8) 1.45e-15
25	294	8.2	391	7	R39260	Murine somatostatin r 2.17e-15
26	294	8.2	391	7	R39259	Human somatostatin re 2.17e-15
27	293	8.2	397	13	R66923	Human C140 receptor 2.65e-15
28	293	8.2	398	13	R66921	Human C140 receptor. 2.65e-15
29	291	8.1	339	10	R53752	Seven transmembrane r 3.95e-15
30	292	8.1	358	6	R28274	Sequence in a low af 3.24e-15
31	292	8.1	372	5	R27793	New platelet factor 4 3.24e-15
32	292	8.1	372	12	R68813	Human lymphocyte PF4A 3.24e-15
33	291	8.1	380	14	R72591	Mammalian kappa opioi 3.95e-15
34	291	8.1	380	13	R67669	Mouse kappa opiod re 3.95e-15
35	291	8.1	380	14	R76783	Rat kappa opiate rece 3.95e-15
36	277	7.7	369	7	R39261	Human somatostatin re 6.46e-14
37	275	7.7	369	7	R39262	Murine somatostatin r 9.61e-14
38	275	7.7	372	14	R76782	Rat delta opiate rece 9.61e-14
39	273	7.6	367	13	R71968	Mouse opiod receptor. 1.43e-13
40	273	7.6	367	13	R67671	Mouse opiod receptor. 1.43e-13
41	273	7.6	369	5	R27504	Pituitary somatostati 1.43e-13
42	272	7.6	371	10	R66503	Murine delta opiod r 1.74e-13
43	272	7.6	372	13	R67670	Mouse delta opiod re 1.74e-13
44	272	7.6	372	9	R48629	Sequence of murine de 1.74e-13
45	270	7.5	358	10	R53745	Partial sequence of s 2.59e-13

ALIGNMENTS

RESULT 1
ID R53751 standard; Protein; 377 AA.
AC R53751;
DT 07-FEB-1995 (first entry)
DE Seven transmembrane receptor (R2).
KW Primer; seven transmembrane receptor; receptor; amplification.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 41..69
FT /label= Transmembrane domain.
FT Domain 77..104
FT /label= Transmembrane domain.
FT Domain 120..138
FT /label= Transmembrane domain.
FT Domain 161..186
FT /label= Transmembrane domain.
FT Domain 207..226
FT /label= Transmembrane domain.
FT Domain 247..270
FT /label= Transmembrane domain.
FT Domain 294..318
FT /label= Transmembrane domain.
PN WO9412635-A.
PD 09-JUN-1994.
PF 17-NOV-1993; U11153.
PR 17-NOV-1992; US-977452.
PA (ICOS-) ICOS CORP.

PI	Godiska R, Gray PW, Schweickart VL;
DR	WPI; 94-200264/24.
DR	N-PSDB; 066177.
DR	DNA encoding seven trans:membrane receptors - used to develop
PT	prods. for use as therapeutic or diagnostic agents for conditions
PT	involving the receptors.
PS	Example 10; Page 77-78; 100pp; English.
CC	PCR using two primers (066174, 066175) was performed to amplify a
CC	partial sequence of the R20 seven transmembrane coding sequence
CC	which was later used as a probe for isolating the R20 genomic clone
CC	(066176) from a human placenta DNA library. During the isolation
CC	of the R20 gene, two weakly hybridising sequences were identified
CC	which had significant homology to other seven transmembrane
CC	receptors. The probe was used to screen a human genomic foetal
CC	liver DNA library, and while the R20 gene could not be identified in
CC	this library, several weakly hybridising clones were plaque
CC	purified, subcloned and sequenced. The two clones were designated
CC	R2 and R12 (066178). This is the sequence encoded by the R2 clone.
SO	Sequence 377 AA;

	Query Match	10.9%; Score 390; DB 10; Length 377;
	Best Local Similarity	40.4%; Pred. No. 7.17e-24;
	Matches	57; Conservative 42; Mismatches 40; Indels 2; Gaps 2;
D b	44 llaillavallvgpnsvfwsilkrmqkrsvtalmvlnlaladlavlltapfflhfl	103
	: : :::: :: :: :::: :: :: :: :: :: :: :: :: :: ::	:
Q y	24 ILSWVLSLTFLGLPGENGLVLWAGLKMQ-RVTNWFHLTLADLLCCLSIASFIAH	82
D b	104 a-dgtwsglacrclchyycgvmysvaevlitamslrdslarvpvsqklrtkamrv	162
	:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	:
Q y	83 ALQGOMPGRFCLKLIPSVIINMFGSFTALTSIDRCRLVFKPICWNHRNVGMACSI	142
D b	163 lagiwlsflllatpvlayrvtv	183
	: : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	:
Q y	143 CGCIWWAFVICPVFYREI	163

RESULT	2	
ID	R44531	standard; Protein; 359 AA.
AC	R44531;	
DT	24-JUN-1994	(first entry)
DE	Human angiotensin II type 1 receptor.	
KW	Angiotensin; Ang II; receptor; antagonist; hypertension.	
OS	Homo sapiens.	
Key	Location/Qualifiers	
FT	Protein	187..313
FT	/note= "claim 1"	
PN	CA2093495-A.	
PD	08-OCT-1993.	
PF	06-APR-1993; 093495.	
PR	07-APR-1992; JP-085445.	
PR	21-APR-1992; JP-101393.	
PR	17-FEB-1993; JP-027835.	
PA	(TAKE) TAKEDA CHEM IND LTD.	
PI	Fujisawa Y, Konishi H, Kuroda S;	
DR	WPI; 94-000128/01.	
DR	N-PSDB; 053486.	
PT	Human angiotensin II type 1 receptor polypeptide - useful	
PT	determining human angiotensin II type 1 receptor antagonist	
PT	activity	
PS	Claim 2; Fig 1; 42pp; English.	
CC	Human Ang II type 1 receptor is useful for determining t	
CC	bioactivity of angiotensin II type 1 receptor antagonist	
CC	useful for treating hypertension. The Ang I type 1 rec	

[illegible]

RESULT	3	
ID	R53753 standard; Protein; 337 AA.	
AC	R53753;	
DT	07-FEB-1995 (first entry)	
DE	Seven transmembrane receptor (RM3).	
KW	Primer; seven transmembrane receptor; receptor; amplification; PCR;	
KW	polymerase chain reaction.	
OS	Homo sapiens.	
OS	Location/Qualifiers	
FH	48..69	
FT	Domain	
FT	/label= Transmembrane domain.	
FT	Domain	
FT	/label= Transmembrane domain.	
FT	Domain	
FT	/label= Transmembrane domain.	
FT	Domain	
FT	/label= Transmembrane domain.	
FT	Domain	
FT	/label= Transmembrane domain.	
FT	Domain	
FT	/label= Transmembrane domain.	
FT	Domain	
FT	/label= Transmembrane domain.	
FT	Domain	
FT	/label= Transmembrane domain.	
FT	Domain	
FT	/label= Transmembrane domain.	
PN	W09412635-A.	
PD	09-JUN-1994.	
PF	17-NOV-1993; U01153.	
PR	17-NOV-1992; US-977452.	
PA	(ICOS-) ICOS CORP.	
PI	Godiska R, Gray PW, Schweickart VI;	
DR	WPI; 94-200264/24.	
DR	N-PSDB; Q66179.	
PT	DNA encoding seven transmembrane receptors - used to develop	
PT	prods. for use as therapeutic or diagnostic agents for conditions	
PT	involving the receptors.	
PS	Example 11; Page 84-85; 100pp; English.	
CC	Two primers (Q66148, Q66149) were used in a PCR reaction containing	
CC	human macrophage cDNA library in plasmid pRC/CMV. When the PCR	
CC	products were subjected to agarose gel electrophoresis a faint band	
CC	of 180-200 base pairs was observed. Re-amplified material was	
CC	digested with BamHI and HindIII and cloned into the plasmid	
CC	Bluescript SK-. Of sixteen clones sequenced, two contained a unique	
CC	sequence termed RM3. Specific primers for the partial RM3 clone were	
CC	used to identify a full length RM3 cDNA clone (Q66179) which	

CC oligonucleotide (Q30015). This probe was designed based on the
CC sequence derived from the second transmembrane domain of G-protein-
CC coupled receptors. After tertiary screening, six plaques were
CC isolated. The insert of one of these plaques, termed F3R was of 2.5
CC kb in size. This insert was sequenced. The protein deduced from
CC the F3R clone demonstrates that it belongs to the family of
CC G-protein-coupled receptors. The deduced protein sequence
CC indicates seven putative transmembrane segments. A human
CC peripheral blood leukocyte lambda gt10 cDNA library (5' stretch) was
CC screened with a 652 bp EcoRI/BamHI fragment (including nucleotides
CC -271 to 625) of the rabbit F3R clone. After tertiary screening
CC several human clones which hybridized to the rabbit IL-8 probe
CC were isolated. The insert of one such clone, termed 4AB was
CC sequenced (Q30012).
CC Sequence 360 AA;
SO

Query Match 9.3%; Score 335; DB 6; Length 360;
Best Local Similarity 32.0%; Pred. No. 5.53e-19;
Matches 48: Conservative 49: Mismatches 47: Indels 6; Gaps 6;

```

Db 52 viiyaivfllsllgnslvmlvilsyrvgrsvtdvyllnlsladllfalf.tpi.waas-kvm 110
      :: | | | | | | | | | | :: | | | | | | | | | | | | | | | | | | |
Ov 27 mvttisltelgpgngvltwvagi-km0rvtvntfwtflttadllcclslafslahlaio 85

```

```

Db      111  g-wifgtfclkwslkvevnfygilllaciisvdyrlaivhatrtltqky-lvkfcls 168
      | | : ||||:: : : : ::||: ||: || : : : : ||
Ou      96  coapvcpefckltpstlvinmefsvelltaistordcivwkdwtconhrnvcmacstgcg 145

```

```

Db      169 iwglslallalpvlfrftvyssnvspac-y 197
      || :||:| :||:| :||:| :||:| :||:| :||:|
Ov      146 iwwafvclcpfvfyr-eiftdnhrccg 174

```

RESULT

ID R70124 standard; Protein; 1064 AA.

DT	14-FEB-1996	(first entry)
DE	IL8-R type 2-GBP 130 fusion protein.	
KW	Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; glycoprotein receptor; glycoprotein binding peptide 130; GBP 130; GBPH; glycoprotein binding peptide homologue; glycophorin A.	
OS	Chimeric Homo sapiens.	
OS	Chimeric Plasmodium falciparum.	
PN	W09506737-A.	
PD	09-MAR-1995.	
PF	01-SEP-1994; G01900.	
PR	03-SEP-1993; GB-018350.	
PR	23-AUG-1994; GB-017021.	
PA	(PREN/) PRENDERGAST K F.	
PI	Prendergast KF;	
DR	WPI; 95-115452/15.	
PT	New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell and a receptor peptide.	
PT	Example A; Page 80-82; 93pp; English.	
PS	Hybrid peptides for binding cytokines, comprising a malaria parasite (Plasmodium falciparum) peptide (capable of binding to a red blood cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples of these hybrid peptides. R70124 is a fusion of interleukin 8 receptor type 2 and glycoprotein binding protein (GBP) 130. The use of cytokine receptors not normally found on RBCs means that the cytokine can bind harmlessly to the RBC without deleterious effect. The RBC protects the hybrid peptides from excretion from the kidney, and due to steric hindrance prevents the cytokines binding to a receptor in another cell.	

CC GBP 130 or GBPH (GBP homologue) are the pref. malaria parasite peptides
CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),
CC PMSA (pre major merozoite surface antigen) and the Duffy binding
CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
CC bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on
CC the surface of RBCs. The hybrid peptides are thus used to lower
CC the levels of free cytokines in the circulation to reduce pathological
CC damage.
SQ Sequence 1064 AA;

Query Match 9.3%; Score 335; DB 14; Length 1064;

Best Local Similarity 32.0%; Pred. No. 5.53e-19;

Matches 48; Conservative 49; Mismatches 47; Indels 6; Gaps 6;

Db 46 viiyalvlllqslgmvlvlysvrsvtdvllnlaladllfaltlpiwaas-kvn 104

Qy 27 MWLSLFLGLPGNLVWVAGL-KMQRTVNTWFLHLTLADLLCCLSIAHLALQ 85

Db 105 q-wifgtfclkvslkvevfysgilllacisvdrylaivhatrtltqky-lvkfcils 162

Qy 86 GMPYGRFLCKLIPSIIVLNMFSGVFLTLAISLDRCLVFRPIWCQHNHNVGMACSGC 145

Db 163 iwgllallalpvllfrtvyssnvspac-y 191

Qy 146 IWWAFVLCIPFVYR-EIFTTDHNRGGY 174

RESULT 9

ID R28272 standard; Protein; 355 AA.

AC R28272;

DT 04-APR-1993 (first entry)

DE Sequence in a high affinity recombinant rabbit interleukin-8

DE (IL-8) receptor polypeptide in F3R.

KW IL-8 receptor polypeptide; G-protein-coupled receptor.

OS Oryctolagus cuniculus.

PN W09218641-A.

PD 29-OCT-1992.

PF 10-APR-1992; U02977.

PR 10-APR-1991; US-685101.

PR 09-JUL-1991; US-726606.

PR 09-DEC-1991; US-803842.

PA (REPK) REPLICON CORP.

PA (UYBO-) UNIV BOSTON.

PI Navarro J, Thomas KM, Witt DP;

DR WPI; 92-382123/46.

DR N-PSDB; Q30011.

PT Recombinant mammalian interleukin-8 receptor - used for screening

PT interleukin-8 binding antagonists, used to treat inflammation

PS Claim 2; Fig 1; 71pp; English.

CC Rabbit high affinity IL-8 receptor gene was isolated from rabbit

CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to

CC produce a rabbit neutrophil cDNA library. 250,000 recombinant

CC plaques were screened for those which hybridized to an antisense

CC oligonucleotide (Q30015). This probe was designed based on the

CC sequence derived from the second transmembrane domain of G-protein-

CC coupled receptors. After tertiary screening, six plaques were

CC isolated. The insert of one of these plaques, termed F3R was of 2.5

CC kb in size. This insert was sequenced. The protein deduced from

CC the F3R clone demonstrates that it belongs to the family of

CC G-protein-coupled receptors. The deduced protein sequence

CC indicates seven putative transmembrane segments.

SQ Sequence 355 AA;

Query Match

9.2%; Score 331; DB 6; Length 355;

Best Local Similarity 30.9%; Pred. No. 1.25e-18;
Matches 46; Conservative 50; Mismatches 49; Indels 4; Gaps 4;

Db 48 wviyalvlllqslgmvlvlysvrsvtdvllnlamadllfaltlpiw-a-vske 105

Qy 27 MWLSLFLGLPGNLVWVAGL-KMQRTVNTWFLHLTLADLLCCLSIAHLALQ 85

Db 106 kgwifgtfclkvslkvevfysgilllacisvdrylaivhatrtltqkrh-lvkfcilg 164

Qy 86 GMPYGRFLCKLIPSIIVLNMFSGVFLTLAISLDRCLVFRPIWCQHNHNVGMACSGC 145

Db 165 iwalslslslpflfrtvyssnvspvcy 193

Qy 146 IWWAFVLCIPFVYR-EIFTTDHNRGGY 174

RESULT 10

ID R27791 standard; Protein; 350 AA.

AC R27791;

DT 12-MAR-1993 (first entry)

DE Interleukin-8 receptor.

KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;

KW pro-inflammatory cytokine.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 40..67

FT /label= transmembrane

FT /note= "putative"

FT Domain 76..98

FT /label= transmembrane

FT /note= "putative"

FT Domain 112..133

FT /label= transmembrane

FT /note= "putative"

FT Domain 155..174

FT /label= transmembrane

FT /note= "putative"

FT Domain 204..226

FT /label= transmembrane

FT /note= "putative"

FT Domain 243..264

FT /label= transmembrane

FT /note= "putative"

FT Domain 292..312

FT /label= transmembrane

FT /note= "putative"

PN W09217497-A.

PD 15-OCT-1992.

PF 23-MAR-1992; U02317.

PR 29-MAR-1991; US-677211.

PR 19-DEC-1991; US-810782.

PA (GETH) GENENTECH INC.

PI Holmes WE, Lee J, Wood WI;

DR WPI; 92-366191/44.

DR N-PSDB; Q29505.

PT Isolated human platelet factor 4 super-family receptor

PT polypeptide and corresp. antibodies and DNA - useful as

PT diagnostic and screening agents, and for treating inflammation or

PT PF4AR-mediated disorders

PS Claim 7; Fig 2; 78pp; English.

CC A cDNA library constructed from human neutrophil mRNA in the mammalian

CC expression vector pRK5B was transfected into COS-7 cells as pools of

CC 2500 clones. One positive pool from the first 58 transfections was

CC partitioned into smaller pools until a pure clone (pRK5B.i18r1.1)

CC was obtained. The ORF encodes a protein of 350 amino acids which
 CC shares several features with the G-protein coupled receptors of the
 CC rhodopsin superfamily, including 7 hydrophobic (transmembrane)
 CC domains. The IL-8 receptor is a preferred PF4AR superfamily member
 CC of the invention. See also Q29506 and Q37107.
 SQ Sequence 350 AA;

Query Match 9.1%; Score 325; DB 5; Length 350;
 Best Local Similarity 31.3%; Pred. No. 4.21e-18;
 Matches 47; Conservative 46; Mismatches 51; Indels 6; Gaps 6;
 Db 43 iiayalvflslgslmvlvylsvrsvtdvllnlaladllfaltlpiwaas-kvm 101
 Qy 27 MWLSTLFLGLPGNGLVWVAGL-KMORTVNTWFLHLTLADLLCCLSLAFSLAHIAIQ 85
 Db 102 g-wifgtfclkvslkvevfysgilllaciavdylaivhatrtltqkrh-lvkfvelg 159
 Qy 86 GQMPYGRFLCKLIPSIIVLNMGSGVFLTAISLDRCLWVFKP IWCQNHRNVGMCSIC-G 144
 Db 160 c-wglamslpfflfrqayhpnnsqvcy 188
 Qy 145 CIWVAFVLCIPVFVYREIFTTDHNRCGY 174

RESULT 11

ID R68811 standard; Protein; 350 AA.
 AC R68811;
 DT 18-JUL-1995 (first entry)
 DE Interleukin-8 receptor.
 KW Interleukin-8 receptor; IL-8 receptor; PF4AR;
 KW platelet factor superfamily receptor; neutrophil; chemotactic;
 KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
 KW fibrosis; colitis; bronchitis; meningitis; therapeutic.
 OS Homo sapiens.
 PN W09428931-A.
 PD 22-DEC-1994.
 PF 07-JUN-1994; U06380.
 PR 11-JUN-1993; US-076093.
 PA (GETH) GENENTECH INC.
 PI Chuncharapai A, Hebert C, Kim KJ, Lee J;
 DR WPI; 95-036114/05.
 DR N-PSDB; Q80520.
 PT Treatment of inflammatory disorders - by administering an
 PT antibody capable of binding a platelet factor 4 superfamily
 PT receptor polypeptide
 PS Disclosure; Page 51-54; 83pp; English.
 CC A cDNA library constructed from human neutrophil mRNA in pRKS5B was
 CC transfected into COS-7 cells, and the cells were screened with 125I-
 CC IL-8. The DNA sequence of isolated cDNA clone pRKS5B.118r1.1,
 CC encoding human IL-8 receptor, is given in Q80520 and the predicted
 CC amino acid sequence in R68811. The receptor is used to raise
 CC antibodies that neutralize the activity of PF4AR, e.g. IL-8 receptor.
 SQ Sequence 350 AA;

Query Match 9.1%; Score 325; DB 12; Length 350;
 Best Local Similarity 31.3%; Pred. No. 4.21e-18;
 Matches 47; Conservative 46; Mismatches 51; Indels 6; Gaps 6;
 Db 43 iiayalvflslgslmvlvylsvrsvtdvllnlaladllfaltlpiwaas-kvm 101
 Qy 27 MWLSTLFLGLPGNGLVWVAGL-KMORTVNTWFLHLTLADLLCCLSLAFSLAHIAIQ 85
 Db 102 g-wifgtfclkvslkvevfysgilllaciavdylaivhatrtltqkrh-lvkfvelg 159
 Qy 86 GQMPYGRFLCKLIPSIIVLNMGSGVFLTAISLDRCLWVFKP IWCQNHRNVGMCSIC-G 144

Qy 86 GQMPYGRFLCKLIPSIIVLNMGSGVFLTAISLDRCLWVFKP IWCQNHRNVGMCSIC-G 144
 Db 160 c-wglamslpfflfrqayhpnnsqvcy 188
 Qy 145 CIWVAFVLCIPVFVYREIFTTDHNRCGY 174

RESULT 12
 ID R70123 standard; Protein; 1060 AA.
 AC R70123;
 DT 14-FEB-1996 (first entry)
 DE IL8-R type 1-GBP 130 fusion protein.
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
 KW red blood cell; cytokine receptor; glycophorin binding peptide 130;
 KW GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
 OS Chimeric Homo sapiens.
 OS Chimeric Plasmodium falciparum.
 PN W09506737-A.
 PD 09-MAR-1995.
 PF 01-SEP-1994; G01900.
 PR 03-SEP-1993; GB-018350.
 PR 23-AUG-1994; GB-017021.
 PA (PREN/) PRENDERGAST K F.
 PI Prendergast KF;
 DR WPI; 95-115452/15.
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a
 PT malaria parasite peptide capable of binding a red blood cell and
 PT a receptor peptide.
 PS Example A; Page 79-80; 93pp; English.
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood
 CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
 CC of these hybrid peptides. R70123 is a fusion of interleukin 8 receptor
 CC type 1 and glycophorin binding protein (GBP) 130. The use of cytokine
 CC receptors not normally found on RBCs means that the cytokine can bind
 CC harmlessly to the RBC without deleterious effect. The RBC protects the
 CC hybrid peptides from excretion from the kidney, and due to steric
 CC hindrance prevents the cytokines binding to a receptor in another cell.
 CC GBP 130 or GBPH (GBP homologue) are the pref. malaria parasite peptides
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),
 CC PMSEA (pre major merozoite surface antigen) and the Duffy binding
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
 CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on
 CC the surface of RBCs. The hybrid peptides are thus used to lower
 CC the levels of free cytokines in the circulation to reduce pathological
 CC damage.
 SQ Sequence 1060 AA;

Query Match 9.1%; Score 325; DB 14; Length 1060;
 Best Local Similarity 31.3%; Pred. No. 4.21e-18;
 Matches 47; Conservative 46; Mismatches 51; Indels 6; Gaps 6;
 Db 43 iiayalvflslgslmvlvylsvrsvtdvllnlaladllfaltlpiwaas-kvm 101
 Qy 27 MWLSTLFLGLPGNGLVWVAGL-KMORTVNTWFLHLTLADLLCCLSLAFSLAHIAIQ 85
 Db 102 g-wifgtfclkvslkvevfysgilllaciavdylaivhatrtltqkrh-lvkfvelg 159
 Qy 86 GQMPYGRFLCKLIPSIIVLNMGSGVFLTAISLDRCLWVFKP IWCQNHRNVGMCSIC-G 144
 Db 160 c-wglamslpfflfrqayhpnnsqvcy 188
 Qy 145 CIWVAFVLCIPVFVYREIFTTDHNRCGY 174

PT antagonists
PS Claim 3; Page 76-77; 94pp; English.
CC The sequences given in R39260, R39262 and R39264 represent the murine
CC somatostatin receptors (SSTR)-1, SSTR-2 and SSTR-3. The DNA encoding
CC these proteins was isolated from total murine pancreatic islet DNA.
CC These DNA sequences may be placed under the control of a suitable
CC promoter and used to transform a host cell. The DNA sequences and
CC these proteins may be used in screening assays for testing candidates
CC including agonists and antagonists of SSTR polypeptides. The assays
CC may be used to discriminate candidate substances with desirable
CC properties specific to SSTR polypeptides. The isolated substances
CC may be used in a wide range of applications eg. diagnosis of various
CC human tumours. Fragments of these DNA sequences may be used as
CC probes in the isolation of other SSTR-encoding clones.
SQ Sequence 428 AA;

Query Match 8.7%; Score 311; DB 7; Length 428;
Best Local Similarity 34.3%; Pred. No. 7.12e-17;
Matches 49; Conservative 41; Mismatches 48; Indels 5; Gaps 5;
Db 46 ilislsvlvc-vvqllqnslyvvv-lrhtsspsvtsvylmlaladelmqlqplflaa 103
Qy ::::| | : :::| |::| | : | : :|::| | | | | | | | | | | | | |
23 VILSWVILSUTFLLGLPGNGLVWVAGLK-MQR-TVNTWFLHLTLADLLCCLSLAFSLA 80
Db 104 qnal-eywpfgeImcrlvmavdginqftsifcltvmavdrylavvhptraarwrtapvar 162
Qy : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
81 HIALAQOMPYGRFLCKLPISIIIVNMFGSVFLTAISLDRLVFKPIWQNHNRVGMAC 140
Db 163 tveravwvasavvlpvvvfsgv 185
Qy : : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
141 SICGCIWVAFVILCIPVFVREI 163

RA	PEREZ H.D., HOLMES R., KELLY E., MCCLARY J., ANDREWS W.H.;
RL	GENE 118:303-304(1992).
[3]	
RN	SEQUENCE FROM N.A.
RP	TISSUE=GRANULOCYTE;
RC	92246937
RM	
RA	YE R.D., CAVANAGH S.L., QUEHENBERGER O., PROSSNITZ E.R.,
RL	COCHRANE C.G.;
RA	BIOCHEM. BIOPHYS. RES. COMMUN. 184:582-589(1992).
[4]	
RN	SEQUENCE FROM N.A.
RP	92218423
RM	
RA	MURPHY P.M., OZCELIK T., KENNEY R.T., TIFFANY H.L., MCDERMOTT D.,
RL	J. BIOL. CHEM. 267:7637-7643(1992).
RA	FRANCKE U.;
CC	-I- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHONYL PEPTIDES,
CC	WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
CC	FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
CC	RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
CC	PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC	-II- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL; M76672; HSFLPX.
DR	EMBL; X63819; HSPRHO.
DR	EMBL; M88107; HSP39A.
DR	EMBL; M84562; HSFPRLIA.
DR	PIR; JC1258; JC1258.
DR	PIR; A42492; A42492.
DR	PIR; JQ1521; JQ1521.
DR	PIR; B42009; B42009.
DR	GCRDB; GCR_0248; -.
DR	GCRDB; GCR_0398; -.
DR	GCRDB; GCR_0406; -.
DR	GCRDB; GCR_0413; -.
DR	MIM; I36539; 11TH EDITION.
DR	PROSITE; PS00237; G-PROTEIN RECEPTOR.
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW	CHEMOTAXIS.
FT	DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 28 50 1 (POTENTIAL).
FT	DOMAIN 51 61 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 62 83 2 (POTENTIAL).
FT	DOMAIN 84 100 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 101 121 3 (POTENTIAL).
FT	DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 141 162 4 (POTENTIAL).
FT	DOMAIN 163 205 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 206 226 5 (POTENTIAL).
FT	DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 243 266 6 (POTENTIAL).
FT	DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 287 306 7 (POTENTIAL).
FT	DOMAIN 307 351 CYTOPLASMIC (POTENTIAL).
FT	CARBHYD 4 4 POTENTIAL.
FT	DISEULFID 98 176 POTENTIAL.
FT	CONFLICT 339 339 S -> C (IN REF. 1).
SQ	SEQUENCE 351 AA; 38964 MW; 677967 CN;

```
Query Match      16.1%; Score 579; DB 3; Length 351;
Best Local Similarity 46.5%; Pred. No. 1.67e+90;
Matches          72; Conservative 43; Mismatches 39; Indels 1; Gaps 1;

Db               27 ilplvlgvtfgvlgnglvwagfrmtvtcttcylnlaldstafatpfllvmsa 86
|||||:|||||: |||||:|||||: ||| |:|:|:|:|: |::| :|:
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QY	24	ILSNVLSLTFELGIPGNGVLVWAGIKMQRTVNTWFLHLTLADLLCCLSLAFSLAHIA	83																																																																																																																																																																												
Db	87	mgekwpfgwglekkihivvdiinlfgvflgicldrcicvlhpywagmhrtvslamkvi	146																																																																																																																																																																												
QY	84	LQGNPQYGRFLCKLPSIIVINMGFSVFLTAISDRCLVWFKPITWQNHNVGMACSIC	143																																																																																																																																																																												
Db	147	vgpwilaivltpvflfittvtimgdyctcfna	181																																																																																																																																																																												
QY	144	GCIIWVAFVLCIPFVYREIFETTDNHR-CGKFG	177																																																																																																																																																																												
<p>RESULT 4</p> <table border="0"> <tr> <td>ID</td><td>C5AR_MOUSE</td><td>STANDARD;</td><td>PRT; 347 AA.</td></tr> <tr> <td>DT</td><td>P30993;</td><td></td><td></td></tr> <tr> <td>DT</td><td>01-JUL-1993</td><td>(REL. 26, CREATED)</td><td></td></tr> <tr> <td>DT</td><td>01-JUL-1993</td><td>(REL. 26, LAST SEQUENCE UPDATE)</td><td></td></tr> <tr> <td>DT</td><td>01-JUL-1993</td><td>(REL. 26, LAST SEQUENCE UPDATE)</td><td></td></tr> <tr> <td>DE</td><td>C5A</td><td>ANAPHYLATOXIN CHEMOTACTIC RECEPTOR (C5A-R).</td><td></td></tr> <tr> <td>GN</td><td>C5AR.</td><td></td><td></td></tr> <tr> <td>OS</td><td>MUS MUSCULUS (MOUSE).</td><td></td><td></td></tr> <tr> <td>OC</td><td>EUKARYOTA; METAZOA;</td><td>CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;</td><td></td></tr> <tr> <td>OC</td><td>EUTHERIA; RODENTIA.</td><td></td><td></td></tr> <tr> <td>RP</td><td>[1]</td><td></td><td></td></tr> <tr> <td>RN</td><td>SEQUENCE FROM N.A.</td><td></td><td></td></tr> <tr> <td>RM</td><td>93017861</td><td></td><td></td></tr> <tr> <td>RL</td><td>GERARD C., BAO L., OROZCO O., PEARSON M., KUNZ D., GERARD N.P.;</td><td></td><td></td></tr> <tr> <td>RA</td><td>J. IMMUNOL. 149:2600-2606(1992).</td><td></td><td></td></tr> <tr> <td>CC</td><td>-!- FUNCTION: RECEPTOR FOR THE CHEMOTACTIC AND INFLAMMATORY PEPTIDE ANAPHYLATOXIN C5. THIS RECEPTOR STIMULATES CHEMOTAXIS, GRANULE ENZYME RELEASE AND SUPEROXIDE ANION PRODUCTION.</td><td></td><td></td></tr> <tr> <td>CC</td><td>-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.</td><td></td><td></td></tr> <tr> <td>CC</td><td>-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.</td><td></td><td></td></tr> <tr> <td>DR</td><td>EMBL; L05630; MMS5AGPR.</td><td></td><td></td></tr> <tr> <td>DR</td><td>EMBL; S46665; S46665.</td><td></td><td></td></tr> <tr> <td>DR</td><td>CCRDB; GCR 0464; -.</td><td></td><td></td></tr> <tr> <td>DR</td><td>CCRDB; GCR 0618; -.</td><td></td><td></td></tr> <tr> <td>DR</td><td>PROSITE; P500237; G. PROTEIN RECEPTOR.</td><td></td><td></td></tr> <tr> <td>KW</td><td>G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;</td><td></td><td></td></tr> <tr> <td>KW</td><td>CHEMOTAXIS.</td><td></td><td></td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>1 33</td><td>EXTRACELLULAR (POTENTIAL).</td></tr> <tr> <td>FT</td><td>TRANSMEM</td><td>34 56</td><td>1 (POTENTIAL).</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>57 67</td><td>CYTOPLASMIC (POTENTIAL).</td></tr> <tr> <td>FT</td><td>TRANSMEM</td><td>68 90</td><td>2 (POTENTIAL).</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>91 106</td><td>EXTRACELLULAR (POTENTIAL).</td></tr> <tr> <td>FT</td><td>TRANSMEM</td><td>107 128</td><td>3 (POTENTIAL).</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>129 149</td><td>CYTOPLASMIC (POTENTIAL).</td></tr> <tr> <td>FT</td><td>TRANSMEM</td><td>150 170</td><td>4 (POTENTIAL).</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>171 197</td><td>EXTRACELLULAR (POTENTIAL).</td></tr> <tr> <td>FT</td><td>TRANSMEM</td><td>198 223</td><td>5 (POTENTIAL).</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>224 239</td><td>CYTOPLASMIC (POTENTIAL).</td></tr> <tr> <td>FT</td><td>TRANSMEM</td><td>240 262</td><td>6 (POTENTIAL).</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>263 279</td><td>EXTRACELLULAR (POTENTIAL).</td></tr> <tr> <td>FT</td><td>TRANSMEM</td><td>280 300</td><td>7 (POTENTIAL).</td></tr> <tr> <td>FT</td><td>DOMAIN</td><td>301 347</td><td>CYTOPLASMIC (POTENTIAL).</td></tr> <tr> <td>FT</td><td>DISULFID</td><td>105 184</td><td>BY SIMILARITY.</td></tr> <tr> <td>FT</td><td>CARBOHYD</td><td>2</td><td>POTENTIAL.</td></tr> <tr> <td>SQ</td><td>SEQUENCE</td><td>347 AA;</td><td>38510 MW; 682838 CN;</td></tr> </table>				ID	C5AR_MOUSE	STANDARD;	PRT; 347 AA.	DT	P30993;			DT	01-JUL-1993	(REL. 26, CREATED)		DT	01-JUL-1993	(REL. 26, LAST SEQUENCE UPDATE)		DT	01-JUL-1993	(REL. 26, LAST SEQUENCE UPDATE)		DE	C5A	ANAPHYLATOXIN CHEMOTACTIC RECEPTOR (C5A-R).		GN	C5AR.			OS	MUS MUSCULUS (MOUSE).			OC	EUKARYOTA; METAZOA;	CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		OC	EUTHERIA; RODENTIA.			RP	[1]			RN	SEQUENCE FROM N.A.			RM	93017861			RL	GERARD C., BAO L., OROZCO O., PEARSON M., KUNZ D., GERARD N.P.;			RA	J. IMMUNOL. 149:2600-2606(1992).			CC	-!- FUNCTION: RECEPTOR FOR THE CHEMOTACTIC AND INFLAMMATORY PEPTIDE ANAPHYLATOXIN C5. THIS RECEPTOR STIMULATES CHEMOTAXIS, GRANULE ENZYME RELEASE AND SUPEROXIDE ANION PRODUCTION.			CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			DR	EMBL; L05630; MMS5AGPR.			DR	EMBL; S46665; S46665.			DR	CCRDB; GCR 0464; -.			DR	CCRDB; GCR 0618; -.			DR	PROSITE; P500237; G. PROTEIN RECEPTOR.			KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;			KW	CHEMOTAXIS.			FT	DOMAIN	1 33	EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM	34 56	1 (POTENTIAL).	FT	DOMAIN	57 67	CYTOPLASMIC (POTENTIAL).	FT	TRANSMEM	68 90	2 (POTENTIAL).	FT	DOMAIN	91 106	EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM	107 128	3 (POTENTIAL).	FT	DOMAIN	129 149	CYTOPLASMIC (POTENTIAL).	FT	TRANSMEM	150 170	4 (POTENTIAL).	FT	DOMAIN	171 197	EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM	198 223	5 (POTENTIAL).	FT	DOMAIN	224 239	CYTOPLASMIC (POTENTIAL).	FT	TRANSMEM	240 262	6 (POTENTIAL).	FT	DOMAIN	263 279	EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM	280 300	7 (POTENTIAL).	FT	DOMAIN	301 347	CYTOPLASMIC (POTENTIAL).	FT	DISULFID	105 184	BY SIMILARITY.	FT	CARBOHYD	2	POTENTIAL.	SQ	SEQUENCE	347 AA;	38510 MW; 682838 CN;
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FT	DOMAIN	57 67	CYTOPLASMIC (POTENTIAL).																																																																																																																																																																												
FT	TRANSMEM	68 90	2 (POTENTIAL).																																																																																																																																																																												
FT	DOMAIN	91 106	EXTRACELLULAR (POTENTIAL).																																																																																																																																																																												
FT	TRANSMEM	107 128	3 (POTENTIAL).																																																																																																																																																																												
FT	DOMAIN	129 149	CYTOPLASMIC (POTENTIAL).																																																																																																																																																																												
FT	TRANSMEM	150 170	4 (POTENTIAL).																																																																																																																																																																												
FT	DOMAIN	171 197	EXTRACELLULAR (POTENTIAL).																																																																																																																																																																												
FT	TRANSMEM	198 223	5 (POTENTIAL).																																																																																																																																																																												
FT	DOMAIN	224 239	CYTOPLASMIC (POTENTIAL).																																																																																																																																																																												
FT	TRANSMEM	240 262	6 (POTENTIAL).																																																																																																																																																																												
FT	DOMAIN	263 279	EXTRACELLULAR (POTENTIAL).																																																																																																																																																																												
FT	TRANSMEM	280 300	7 (POTENTIAL).																																																																																																																																																																												
FT	DOMAIN	301 347	CYTOPLASMIC (POTENTIAL).																																																																																																																																																																												
FT	DISULFID	105 184	BY SIMILARITY.																																																																																																																																																																												
FT	CARBOHYD	2	POTENTIAL.																																																																																																																																																																												
SQ	SEQUENCE	347 AA;	38510 MW; 682838 CN;																																																																																																																																																																												

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Query Match      15.5%; Score 555; DB 1; Length 347;
Best local Similarity 42.9%;
Pred. No. 1.63e-85;
Matches 70; Conservative 46; Mismatches 45; Indels 2; Gaps 1;

Db 27 ptkrpgdvaalliyvfvvgpgnalvwrtafepdgsnaiwflnvlavdlslclamp 86
| | : : : : | : | : | : | : | : | : : : : : | : | : | : | : | : | : : :

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QY	17	P	NHNEP	P	V	L	S	W	I	S	T	F	L	G	P	G	N	G	L	U	V	A	G	L	K	M	O	R	T	W	I	N	F	L	H	L	T	L	A	D	L	J	C	C	S	L	A	76					
Db	87	V	L	F	T	V	L	N	H	N	Y	W	F	D	A	T	A	C	I	P	S	L	L	I	N	M	A	S	I	L	L	A	T	A	S	A	D	F	L	L	V	K	P	I	W	C	A	K	V	R	G	T	146
QY	77	F	S	L	A	L	A	L	Q	O	M	P	Y	G	R	F	L	K	L	P	S	I	T	V	L	N	F	G	S	V	L	T	A	I	S	D	R	C	L	V	F	K	P	I	W	C	O	N	H	R	N	V	136
Db	147	G	L	A	M	A	C	G	A	V	W	L	L	L	T	P	S	Y	R	E	A	Y	K	D	F	S	E	H	T	W	C	G	I	N	G	Y	189																
QY	137	G	M	A	C	S	I	C	T	G	A	V	F	V	L	G	I	P	V	F	Y	E	I	F	T	--	D	N	H	N	C	K	G	Y	F	E	177																

FT	DISULFID	98	176	POTENTIAL.
FT	CONFLICT	94	94	A -> G (IN REF. 2).
FT	CONFLICT	211	211	T -> S (IN REF. 2).
FT	CONFLICT	338	338	H -> D (IN REF. 2).
SQ	SEQUENCE	353 AA;	40015 MW;	689682 CN;
Query Match		15.4%;	Score 553;	DB 3; Length 353;
Best Local Similarity		40.0%;	Pred. No. 4,24e-85;	
Matches	72;	Conservative	56;	Mismatches 49;
				Indels 3; Gaps 3;

ID	AC2R_MELGA	STANDARD;	PRT;	359 AA.
AC	P33396;			
DT	01-FEB-1994 (REL. 28, CREATED)			
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)			
DE	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	TYPE-1 ANGIOTENSIN II RECEPTOR (AT1).			
OS	MELEAGRIS GALLOPAVO (COMMON TURKEY).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;			
OC	GALLIFORMES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=ADRENAL GLAND;			
RM	93341466			
RA	MURPHY T.J., NAKAMURA Y., TAKEUCHI K., ALEXANDER R.W.;			
RL	MOL. PHARMACOL. 44;1-7(1993).			
CC	-!- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY			
CC	ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-			
CC	CALCIUM SECOND MESSENGER SYSTEM.			
CC	-!- TISSUE SPECIFICITY: ADRENAL MEDULLA.			
CC	-!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL; L23203; MCANAE.			
DR	GCRCB; GCR_0681; -.			
DR	GCRCB; GCR_0758; -.			
DR	PROSITE; PS00237; G PROTEIN RECEPTOR.			
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.			
FT	DOMAIN 1 27	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 28 52	1 (POTENTIAL).		
FT	DOMAIN 53 64	CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 65 87	2 (POTENTIAL).		
FT	DOMAIN 88 102	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 103 124	3 (POTENTIAL).		
FT	DOMAIN 125 142	CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 143 162	4 (POTENTIAL).		
FT	DOMAIN 163 192	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 193 214	5 (POTENTIAL).		
FT	DOMAIN 215 240	CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 241 262	6 (POTENTIAL).		
FT	DOMAIN 263 275	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 276 296	7 (POTENTIAL).		
FT	DOMAIN 297 359	CYTOPLASMIC (POTENTIAL).		
FT	CARBOHYD 4 4	POTENTIAL.		
FT	CARBOHYD 176 176	POTENTIAL.		
FT	CARBOHYD 187 187	POTENTIAL.		
FT	CARBOHYD 188 188	POTENTIAL.		
FT	DISULEID 101 180	BY SIMILARITY.		
SQ	SEQUENCE 359 AA; 41250 MW; 732730 CN;			

Query Match 10.9%; Score 391; DB 1; Length 359;
Best Local Similarity 38.2%; Pred. No. 4.50e-52;
Matches 60; Conservative 46; Mismatches 46; Indels 5; Gaps 4;

	Query match	Score	Score %	Length
Best local Similarity	38.2%	Pred. No. 4,50e-52;		
Matches	60;	Conservative	46;	Mismatches 46; Indels 5; Gaps
Db	29	imvptysiiifiqifgnslvviycymklktvasiflnlaladl-cflitlplwaa	87	
		: : : : : : : : : : : : : : : : : :		
Qy	24	ILSWILSTLTFLGPGNGVLWVA-GIMQRTVNTTWELHUTLADLLCCL-SLAFSLAH	81	
Db	88	tameyqwpfncncklaaagisfnlyasvfltlclsidrylaihpvpykrrrtmfavrv	147	
		:: : : : : : : : : : : : : : : : :		
Qy	82	LALQGOOMPVGREFLCKLIPSLIVINMGCSVFLITAI SLDRCLVKEKPTWCQNHNVGMACS	141	
Db	148	tcviwllagvaslpwihrniffaenlmtvcgfr	184	
		: : : : : : : : : : : : : : : :		
Qy	142	ICGCIWNAFVLCIPFVYVREIFTDHNHR--CGYKF	176	

142 ICGIWWAFVLCIPFVYREIFTTDNHR--CGYK 176

RESULT 10
 ID AG2R XENIA STANDARD; PRT; 362 AA.
 AC P32303;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE TYPE-1-LIKE ANGIOTENSIN II RECEPTOR 1 (AT1).
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EKURAYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 93343933
 RA JI H., SANDBERG K., ZHANG Y., CATT K.J.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 194:756-762 (1993).
 CC -/- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -/- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -/- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; L16463; XLANG2R.
 DR GCRDB; GCR 0693; -.
 DR PROSITE; P500237; G-PROTEIN RECEPTOR.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; LIPOPROTEIN;
 KW PALMITATE; PHOSPHORYLATION.
 FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 53 1 (POTENTIAL).
 FT DOMAIN 54 65 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 66 88 2 (POTENTIAL).
 FT DOMAIN 89 103 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 104 125 3 (POTENTIAL).
 FT DOMAIN 126 143 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 144 163 4 (POTENTIAL).
 FT DOMAIN 164 193 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 194 215 5 (POTENTIAL).
 FT DOMAIN 216 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 261 6 (POTENTIAL).
 FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 275 295 7 (POTENTIAL).
 FT DOMAIN 296 362 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 3 3 POTENTIAL.
 FT CARBOHYD 18 18 POTENTIAL.
 FT CARBOHYD 177 177 POTENTIAL.
 FT DISULFID 102 181 BY SIMILARITY.
 FT LIPID 361 PALMITATE (POTENTIAL).
 SQ SEQUENCE 362 AA; 41039 MW; 735750 CN;

Query Match 10.3%; Score 369; DB 1; Length 362;
 Best Local Similarity 35.6%; Pred. No. 1.05e-47;
 Matches 52; Conservative 48; Mismatches 40; Indels 6; Gaps 6;
 Db 28 ifiaipiytstifvqvgfmsvviyvsymkm-ktvasiflmmlalsdl-cfvitiplw 85
 QY 23 VILSM-VTLSTFLGIPGNGULVWA-G-LKQRTVNTWFLHLLTLADLLC-CLSLAFS 78
 Db 86 aaytamhywpfnflekvaataitlnlyttvfltlclsidrysaivhpmksriwtanv 145
 QY 79 LAHLAQCOMPYGRFLCKLIPSIIVLNMFSGVELLTAISLDRLVFKPIWQCNHRNVGM 138
 Db 146 arltcvgiwlvaflaemspiiyrqiy 171
 QY 139 ACSICGCIWVAVVICIPVYREIF 164

RESULT 11
 ID AG2S XENIA STANDARD; PRT; 363 AA.
 AC P35373;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE TYPE-1-LIKE ANGIOTENSIN II RECEPTOR 2 (AT1).
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EKURAYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RM 93360920
 RA BERGSMAN D.J., ELLIS C., NUTHULAGANTI P.R., NAMBI P., SCAIFE K.,
 RA ROMAR C., AIYAR N.;
 RL MOL. PHARMACOL. 44:277-284 (1993).
 CC -/- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY
 CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -/- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -/- TISSUE SPECIFICITY: HEART MEMBRANES, FOLLICULAR OOCYTES.
 CC -/- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U01155; XLI55.
 DR GCRDB; GCR 0763; -.
 DR PROSITE; P500237; G-PROTEIN RECEPTOR.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; LIPOPROTEIN;
 KW PALMITATE; PHOSPHORYLATION.
 FT DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 30 54 1 (POTENTIAL).
 FT DOMAIN 55 66 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 67 89 2 (POTENTIAL).
 FT DOMAIN 90 104 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 105 126 3 (POTENTIAL).
 FT DOMAIN 127 144 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 145 164 4 (POTENTIAL).
 FT DOMAIN 165 194 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 195 216 5 (POTENTIAL).
 FT DOMAIN 217 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 262 6 (POTENTIAL).
 FT DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 296 7 (POTENTIAL).
 FT DOMAIN 297 363 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT DISULFID 103 182 BY SIMILARITY.
 FT LIPID 346 346 PALMITATE (POTENTIAL).
 FT LIPID 362 362 PALMITATE (POTENTIAL).
 SQ SEQUENCE 363 AA; 41540 MW; 745704 CN;

Query Match 10.2%; Score 368; DB 1; Length 363;
 Best Local Similarity 34.4%; Pred. No. 1.65e-47;
 Matches 54; Conservative 51; Mismatches 44; Indels 8; Gaps 8;
 Db 29 ifitipiytstifvqvgfmsvviyvsymkm-ktmasviflmmlalsdl-cfvitiplw 86
 QY 23 VILSM-VTLSTFLGIPGNGULVWA-G-LKQRTVNTWFLHLLTLADLLC-CLSLAFS 78
 Db 87 aaytamhywpfnflekvaataitlnlyttvfltlclsidrysaivhpmksriwtanv 146
 QY 79 LAHLAQCOMPYGRFLCKLIPSIIVLNMFSGVELLTAISLDRLVFKPIWQCNHRNVGM 138

Db	147	artcvegwlavlaflpslvyrqifpdtntqvca	183
	I	I	11:1111: :1 :11:11 I I: I:
Qy	139	ACSGICGHWAVFVLCIPVFVYREIFT-TD-NHNRG	173

RESULT	12	
ID	AC2R HUMAN	STANDARD; PRT; 359 AA.
AC	P30536;	
DT	01-APR-1993 (REL. 25, CREATED)	
DT	01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)	
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)	
DE	TYPE-1A ANGIOTENSIN II RECEPTOR (AT1A).	
GN	AGTR1 OR AT2R1.	
OS	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA;	
OC	EUTHERIA; PRIMATES.	
RN	[1]	SEQUENCE FROM N.A.
RM	92337608	
RA	MAUZY C.A., HWANG O., EGLOFF A.M., WU L.H., CHUNG F.-Z.;	
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 186:277-284(1992).	
RN	[2]	SEQUENCE FROM N.A.
RC	TISSUE=LIMPHOCYTES;	
RM	92181475	
RA	FURUTA H., GUO D.F., INAGAMI T.;	
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 183:8-13(1992).	
RN	[3]	SEQUENCE FROM N.A.
RC	TISSUE=LIVER;	
RM	92231907	
RA	BERGSA D.J., ELLIS C., KUMAR C., NUTHALAGANTI P., KERSTEN H.,	
RA	ELSHOURBAC N.A., GRIFFIN E., STADEL J.M., ATYAR N.;	
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 183:989-995(1992).	
RN	[4]	SEQUENCE FROM N.A.
RC	TISSUE=LIVER;	
RM	92198490	
RA	TAKAYANAGI R., OHNAKA K., SAKAI Y., NAKAO R., YANASE T., HAJI M.,	
RA	INAGAMI T., FURUTA H., GOU D.F., NAKAMURA M., NAWATA H.;	
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 183:910-916(1992).	
RN	[5]	SEQUENCE FROM N.A.
RM	92375105	
RA	CURNOW K.M., PASCOE L., WHITE P.C.;	
RL	MOL. ENDOCRINOL. 6:1113-1118(1992).	
CC	-/- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY	
CC	ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-	
CC	CALCIUM SECOND MESSENGER SYSTEM.	
CC	-/- TISSUE SPECIFICITY: LIVER, LONG, ADRENAL, AND ADRENOCORTICAL	
CC	ADENOMAS.	
CC	-/- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.	
CC	-/- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	
CC	-/- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR	EMBL; M91464; HSATIA.	
DR	EMBL; Z11162; HSANTENII.	
DR	EMBL; M87290; HSANTIR.	
DR	EMBL; M93394; HSANTIIR.	
DR	PIR; A44014; A44014.	
DR	PIR; JC1104; JC1104.	
DR	GCRRB; GCR_0296; -.	
DR	GCRRB; GCR_0384; -.	
DR	GCRRB; GCR_0421; -.	
DR	GCRRB; GCR_0447; -.	

DR	MIM; 106165; 11TH EDITION.
KR	PROSITE; PS00237; G PROTEIN RECEPTOR.
KW	PALMITATE; PHOSPHORYLATION.
FT	DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT	TRANSEM 28 52 1 (POTENTIAL).
FT	DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT	TRANSEM 65 87 2 (POTENTIAL).
FT	DOMAIN 88 102 EXTRACELLULAR (POTENTIAL).
FT	TRANSEM 103 124 3 (POTENTIAL).
FT	DOMAIN 125 142 CYTOPLASMIC (POTENTIAL).
FT	TRANSEM 143 162 4 (POTENTIAL).
FT	DOMAIN 163 192 EXTRACELLULAR (POTENTIAL).
FT	TRANSEM 193 214 5 (POTENTIAL).
FT	DOMAIN 215 240 CYTOPLASMIC (POTENTIAL).
FT	TRANSEM 241 262 6 (POTENTIAL).
FT	DOMAIN 263 275 EXTRACELLULAR (POTENTIAL).
FT	TRANSEM 276 296 7 (POTENTIAL).
FT	DOMAIN 297 359 CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 4 4 POTENTIAL.
FT	CARBOHYD 176 176 POTENTIAL.
FT	CARBOHYD 188 188 POTENTIAL.
FT	DISULFID 101 180 BY SIMILARITY.
FT	LIPID 355 355 PALMITATE (POTENTIAL).
SQ	SEQUENCE 359 AA; 41061 MW; 712927 CN;
 Query Match 9.9%; Score 357; DB 1; Length 359; Best Local Similarity 33.7%; Pred. No. 2.44e-45; Matches 56; Conservative 54; Mismatches 48; Indels 8; Gaps 8;	
Db	27 ifvmiptlysiifvgifgnelvnviyivfymklktvasflnladl-clfltclplwa 85 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy	24 ILSNW-II-STFLIGLPNGVLVAGIKMQ-RVVNTWFLHLTLADIALLCCII-SIAFSI 79 : : : : : : : : : : : : : : : :
Db	86 vytameyrwfpqnylkckiasasfnlyasvflltclsldrylaivhpmarkerlrmtlva 145 : : : : : : : : : : : : : : : :
Qy	80 AHIALGQMPYGRFLKLIPISVIVLNWFSGVELLTALSIDRCGLVVFPEIQCNHRNVGMA 139 : : : : : : : : : : : : : : : :
Db	146 kvtciiilwllaqlaspaiihnrnvffientnitcaphyesgntsl 191 :: : : : : : : : : : : : : : : : :
Qy	140 CSICGCIWWAFVLCIPVEFYREIFTTDNHN-R-CGYKF-GUSSSL 182
RESULT 13	
ID AG2R PIG STANDARD; PRT; 359 AA.	
AC P30555;	
DT 01-APR-1993 (REL. 25, CREATED)	
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)	
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)	
DE TYPE-1 ANGIOTENSIN II RECEPTOR (AT1).	
OS SUS SCROFA (PTG).	
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC EUTHERIA; ARTIODACTYLIA.	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=AORTIC SMOOTH MUSCLE;	
RM 93259232	
RA ITAZAKI K., SHIGERI Y., FUJIMOTO M.;	
RL EUR. J. PHARMACOL. 245:147-156(1993).	
CC -!- FUNCTION: RECEPTOR FOR ANGIOTENSIN II. MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.	
CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.	
CC -!- CELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	

[illegible]

Search completed: Wed May 1 15:31:40 1996
Job time : 37 secs.